

OM nucleic - nucleic search, using sw model

Run on: August 10, 2004, 13:51:42 ; Search time 1294 Seconds
(without alignments)
11966.524 Million cell updates/sec

Title: US-09-875-228-1_COPY_5976_9620
Perfect score: 3645
Sequence: 1 ggcctccataaattgttag.....ggaggagctgtggactggc 3645

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 50.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 150

Total number of hits satisfying chosen parameters: 17

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 250 summaries

Database : N Geneseqn_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query Match	Length	ID	Description				
1	3645	100.0	12047	2	AAV17618 Homo sapi				
2	3645	100.0	12047	2	Aaz06489 Human gla				
3	3645	100.0	12047	3	Aaz99934 DNA seque				
4	3645	100.0	12047	3	AAH46852 Nucleotid				
5	3645	100.0	12047	5	Aah43617 Human gla				
6	3645	100.0	12047	5	Aaf87248 Human gla				
7	3645	100.0	12047	6	Abk9584 Mucin tra				
8	3645	100.0	12047	7	ACD07307 Human gla				
9	3400	93.3	12047	2	Aax24755 Human gla				
10	1172	32.2	1172	2	AAX24772 Human gla				
11	1172	32.2	1172	2	Aaz06494 hKlK2 enh				
12	1114	30.6	1558	3	Aaz94285 Human pro				
13	993	27.2	1172	2	Aax24774 Human gla				
14	993	27.2	1172	2	AAX24773 Human gla				
15	993	27.2	1172	2	Aaz06495 hKlK2 enh				
16	993	27.2	1172	2	Aaz06496 hKlK2 enh				
17	204	5.6	204	5	Aaf82694 Glandular				

ALIGNMENTS

AAV17618

ID AAV17618 standard; DNA; 12047 BP.

XX AAV17618;

AC AAV17618;

XX 25-MAR-2003 (revised)

DT 21-JUL-1998 (first entry)

XX Homo sapiens glandular kallikrein-1 promoter region.

DE

XX Promoter; enhancer; 5' non-coding region; hKlK2; kallikrein; hGK-1; PSA;

KW prostate specific antigen; prostate cancer; treatment; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT enhancer 6859..8627

FT /tag= a

FT /note= "enhancer active fragment"

FT 11420..12047

FT /tag= b

FT /note= "promoter active fragment"

FT 12013..12047

FT /tag= c

FT /note= "transcription initiation at 12013"

XX

PN WO9805797-A1.

XX

PD 12-FEB-1998.

XX

PF 06-AUG-1997; 97WO-US013888.

XX

PR 06-AUG-1996; 96US-00692759.

PR 04-AUG-1997; 97US-00906192.

XX

PA (CALY-) CALYDON.

XX

PI Henderson DR, Schuur ER, Lamparski HG, Yu D;

XX

DR WPI; 1998-145628/13.

XX

PT Screening drugs for treatment of prostate cancer - uses prostate specific antigen expressing cells.

PT

XX Disclosure; Page 25-28; 4pp; English.

XX

CC The sequence is that of the non-coding region of human glandular kallikrein-1 (hKlK2) which contains promoter and enhancer active regions. This transcription initiation regulatory region can be used as part of a method for screening drugs for the treatment of prostate cancer employing prostate specific antigen (PSA) expressing cells comprising an expression construct which comprises a transcriptional initiation region of the PSA enhancer, a promoter and a gene whose expression product provides a detectable signal, where the gene is under the transcriptional control of the initiation region, comprises: (a) combining the PSA expressing cells with a candidate drug in the presence of an androgen for sufficient time for detectable expression of the gene, and (b) detecting the level of expression of the gene as compared to the level of expression in the absence of the candidate drug. The method can be used to evaluate the potential of a compound as a therapeutic agent for the treatment of prostate cancer. Particularly, anti-androgenic activity can be evaluated as indicative of therapeutic effects for prostate cancer, although any compound which modifies the expression of a prostate-specific gene may be considered a candidate compound. (Updated on 25-MAR-2003 to correct PR field.)

CC

Sequence 12047 BP; 3051 A; 2484 C; 2869 G; 3643 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 3645; DB 2; Length 12047;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCTCATAATTTGTAAGAGTGAATGTCCAAAGATGGAATAATGTTGAGAACTA 60

Db 5976 GGCCTCAATAAATGTTAAGAGTGTAAATGTGTCCTAAGATGGAAATGTTTCAGAACTA 6035
Qy 61 CTGTCCAGAGATTTCTCGAGTCTTAGAGTGTGGGAATATAGAACTCGAGCTTGGCTT 120
Db 6036 CTGTCCAGAGATTTCTCGAGTCTTAGAGTGTGGGAATATAGAACTCGAGCTTGGCTT 6095
Qy 121 CTTCAGCTAGATCAGAGATATGGGCTGAAGTCTGAAGCTTGGCTTGAAGTATGG 180
Db 6096 CTTCAGCTAGATCAGAGATATGGGCTGAAGTCTGAAGCTTGGCTTGAAGTATGG 6155
Qy 181 GTTGGCTTCCGAGACATATTTGACATGTTGGGCTGTGATTTGGGTTTGGTATTTGC 240
Db 6156 GTTGGCTTCCGAGACATATTTGACATGTTGGGCTGTGATTTGGGTTTGGTATTTGC 6215
Qy 241 TCTGAATCCTAATGCTGTCTTGAGGCATCTAGAATCTGAAGTCTGAAGTCTGAAGTCT 300
Db 6216 TCTGAATCCTAATGCTGTCTTGAGGCATCTAGAATCTGAAGTCTGAAGTCTGAAGTCT 6275
Qy 301 ATTATCTGTAGTAGGACATCTCCAGTCTCTGTTCTGCTTCTAGGCTGGAGTCTGTAGT 360
Db 6276 ATTATCTGTAGTAGGACATCTCCAGTCTCTGTTCTGCTTCTAGGCTGGAGTCTGTAGT 6335
Qy 361 CAGTGACCCGCTCGGCAATTTCAACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 420
Db 6336 CAGTGACCCGCTCGGCAATTTCAACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 6395
Qy 421 CAACCAACCAACCAATTAACCAATAGAACTTTCCCACTTCCCTAGCTGCAATGTTAA 480
Db 6396 CAACCAACCAACCAATTAACCAATAGAACTTTCCCACTTCCCTAGCTGCAATGTTAA 6455
Qy 481 ACCTAGATTTCTGTTTAAATAGGTTTCAATGAATATTTTCCAGCTCTGATCCAACTTTACAT 540
Db 6456 ACCTAGATTTCTGTTTAAATAGGTTTCAATGAATATTTTCCAGCTCTGATCCAACTTTACAT 5515
Qy 541 TCCTTCTACGCTTATCTCAACCCACTTAAATATGCAATTTCCCAATATATTTCCCTGGATT 600
Db 6516 TCCTTCTACGCTTATCTCAACCCACTTAAATATGCAATTTCCCAATATATTTCCCTGGATT 6575
Qy 601 CTACCTATATGTAATCTGCTGCTTCCAGTCTTCTAGTGCAATTAACATACCTGATTTA 660
Db 6576 CTACCTATATGTAATCTGCTGCTTCCAGTCTTCTAGTGCAATTAACATACCTGATTTA 6635
Qy 661 CATCTTTTAACTTAAAGTGGAATTAAGAGTCTCTGCGAGAGTTCAGAGTCTCAAGA 720
Db 6636 CATCTTTTAACTTAAAGTGGAATTAAGAGTCTCTGCGAGAGTTCAGAGTCTCAAGA 6695
Qy 721 TGGCCCTTACTCTGACATCAATGAGATTTCAAGGAGTTCGCAAGATCATCTCAGT 780
Db 6696 TGGCCCTTACTCTGACATCAATGAGATTTCAAGGAGTTCGCAAGATCATCTCAGT 6755
Qy 781 TCAGTGATGCTGCTAGCTTCAATCAATCAATGAAAGCTGTTTCTGCTCATGGCTATGG 840
Db 6756 TCAGTGATGCTGCTAGCTTCAATCAATCAATGAAAGCTGTTTCTGCTCATGGCTATGG 6815
Qy 841 TTTATTAACAGAAAGATAGATGAAATCTAGCAAGGAGAGTTCATGGGGCAAA 900
Db 6816 TTTATTAACAGAAAGATAGATGAAATCTAGCAAGGAGAGTTCATGGGGCAAA 6875
Qy 901 GACAAGGAGAGCTTCAAGTTCAGAGATTTCTGTTGTTTCTCCAGTGGTGTATGGAAA 960
Db 6876 GACAAGGAGAGCTTCAAGTTCAGAGATTTCTGTTGTTTCTCCAGTGGTGTATGGAAA 6935
Qy 961 GCAGTATCTTCTCCATACAAATGATGTGATATATTCAGTGTATTTGCAATCAGGGAAC 1020
Db 6936 GCAGTATCTTCTCCATACAAATGATGTGATATATTCAGTGTATTTGCAATCAGGGAAC 6995
Qy 1021 TCAACTGAGCTTGTATATTTGAGCTTGGTGTGACAGACATGTCGACACCTTCATGG 1080
Db 6996 TCAACTGAGCTTGTATATTTGAGCTTGGTGTGACAGACATGTCGACACCTTCATGG 7055
Qy 1081 CTGAACCTTATAGTACTTAGCCCTCCAGAGCTTACAGCTGTAGGCTGTAAACCCCAACT 1140

Db 7056 CTGAACCTTATAGTACTTAGCCCTCCAGAGCTCTACAGCTGATAGGCTGTAAACCCCAACT 7115
Qy 1141 GTCCACATAAATCAATTTGTTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 1200
Db 7116 GTCCACATAAATCAATTTGTTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 7175
Qy 1201 GCACCTTAAACAGGAGGATATTTCAAAGCTTTAGAGATGACCTCCAGAGAGCTGAATGC 1260
Db 7176 GCACCTTAAACAGGAGGATATTTCAAAGCTTTAGAGATGACCTCCAGAGAGCTGAATGC 7235
Qy 1261 AAAGACCTTGGGCTCTTTTGGGCAAGGAGATCTCTTTTACCGACACACTCTCTCTCACAGGTT 1320
Db 7236 AAAGACCTTGGGCTCTTTTGGGCAAGGAGATCTCTTTTACCGACACACTCTCTCTCACAGGTT 7295
Qy 1321 ATTGTAGGATCAAAATGTGTCATGTGTGAGACACACAGACATGTCCTGGCTGTGAGA 1380
Db 7296 ATTGTAGGATCAAAATGTGTCATGTGTGAGACACACAGACATGTCCTGGCTGTGAGA 7355
Qy 1381 GTGACTTCTATGTGCTTAACTTGTCTGAGTGTGCTTAAGAAAGTATTAGGCAATGCTTTTCA 1440
Db 7356 GTGACTTCTATGTGCTTAACTTGTCTGAGTGTGCTTAAGAAAGTATTAGGCAATGCTTTTCA 7415
Qy 1441 CACTCACAGATGCTCATCTAACTCTCAACATGGCTTACAGGCTGGGCACTACTAGGCTT 1500
Db 7416 CACTCACAGATGCTCATCTAACTCTCAACATGGCTTACAGGCTGGGCACTACTAGGCTT 7475
Qy 1501 ATTTGACAGAGGAAGGACTGTGATTAAGAGGGGTGACCAATAGTCTAGAGTCAATCT 1560
Db 7476 ATTTGACAGAGGAAGGACTGTGATTAAGAGGGGTGACCAATAGTCTAGAGTCAATCT 7535
Qy 1561 GGATGCAAGGGGCTCCAGAGACCATGATTTAGACATTTGTCTGACAGAAATTTATGGCTGG 1620
Db 7536 GGATGCAAGGGGCTCCAGAGACCATGATTTAGACATTTGTCTGACAGAAATTTATGGCTGG 7595
Qy 1621 ATGTCTCTGCCCCGAAAGGGGATGACATTTCTTGAACCCCTATCTCAGATCTTGACT 1680
Db 7596 ATGTCTCTGCCCCGAAAGGGGATGACATTTCTTGAACCCCTATCTCAGATCTTGACT 7655
Qy 1681 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCCCATATATATCTCTCTGTGTCT 1740
Db 7656 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCCCATATATATCTCTCTGTGTCT 7715
Qy 1741 TCTCCCTTCTCAGTCTTACTGCCCCATCTTCTCCAGCTCCATCTCAGCTGGCAGGTG 1800
Db 7716 TCTCCCTTCTCAGTCTTACTGCCCCATCTTCTCCAGCTCCATCTCAGCTGGCAGGTG 7775
Qy 1801 TAGCCACAGTACCTAACTCTTTGACAGAACTATAAATGTATCTTACAGGAGGAGAAA 1860
Db 7776 TAGCCACAGTACCTAACTCTTTGACAGAACTATAAATGTATCTTACAGGAGGAGAAA 7835
Qy 1861 AAAAAAGAACTCTGAAAGAGCTGACATTTTACCGACTTGCACACATTAAGCTAACCTG 1920
Db 7836 AAAAAAGAACTCTGAAAGAGCTGACATTTTACCGACTTGCACACATTAAGCTAACCTG 7895
Qy 1921 CCAGTTTGTGCTGTTAGAACTCATGAGACTCTGGTCTAGAGCAAAAGATTTTATTAC 1980
Db 7896 CCAGTTTGTGCTGTTAGAACTCATGAGACTCTGGTCTAGAGCAAAAGATTTTATTAC 7955
Qy 1981 CCAGGCTAAGGAGGAGCATGAACCTTTGTTTCAACATTTGTTTCTCTCTCTCTCTCT 2040
Db 7956 CCAGGCTAAGGAGGAGCATGAACCTTTGTTTCAACATTTGTTTCTCTCTCTCTCTCT 8015
Qy 2041 CATATGGGATGATCAGAGGAGTTCAGGTGATGAGACACAGGGGTTTGTGCAAGGTTAG 2100
Db 8016 CATATGGGATGATCAGAGGAGTTCAGGTGATGAGACACAGGGGTTTGTGCAAGGTTAG 8075
Qy 2101 CAACCTAGGCTTAGAAATCTCTAATCTTAAAGAGGTACTAGCAAACTTGTCCAGTCTT 2160
Db 8076 CAACCTAGGCTTAGAAATCTCTAATCTTAAAGAGGTACTAGCAAACTTGTCCAGTCTT 8135
Qy 2161 TGTATCTGACGAGGATATTTCTTTTAAATTTGGGTTGAAAGAGACCTACTCTGGAGGAA 2220
Db 8136 TGTATCTGACGAGGATATTTCTTTTAAATTTGGGTTGAAAGAGACCTACTCTGGAGGAA 8195

Qy 2221 CATATTGTAATTTATGTGCTGAAACAGTAAACAAATCTGCTGTAAATATAGACGTTAACTTT 2280
Db CATATTGTAATTTATGTGCTGAAACAGTAAACAAATCTGCTGTAAATATAGACGTTAACTTT 8255
Qy 2281 ATTATCTAAGGCGAGTAAAGCAACCTAGATCTGAAGCGGATACCATCTTCCAGAGCTATCT 2340
Db ATTATCTAAGGCGAGTAAAGCAACCTAGATCTGAAGCGGATACCATCTTCCAGAGCTATCT 8315
Qy 2341 GCTGTACAAATATGCTTTGAAAGATGGTCCAGAAAAGAAAACGGTATTATTGCTTTGCT 2400
Db GCTGTACAAATATGCTTTGAAAGATGGTCCAGAAAAGAAAACGGTATTATTGCTTTGCT 8375
Qy 2401 CAGAGGACACAGAAACATAAGAGAACCATGGAATAATGCTCCCAACACTGTTCAACC 2460
Db CAGAGGACACAGAAACATAAGAGAACCATGGAATAATGCTCCCAACACTGTTCAACC 8435
Qy 2461 AGAGCCCTTCACCTCTTGTCTGCAAGGACAGTCTTAAACATCCCATATTAGTGTGTACCA 2520
Db AGAGCCCTTCACCTCTTGTCTGCAAGGACAGTCTTAAACATCCCATATTAGTGTGTACCA 8495
Qy 2521 CATCTGCTTCACGCTGCTTAACCAAGATTTCTAGTCCAGTTCCCAACATGTTGGCA 2580
Db CATCTGCTTCACGCTGCTTAACCAAGATTTCTAGTCCAGTTCCCAACATGTTGGCA 8555
Qy 2581 GTGCCCCACTGCCAACCCCAAGATTAAGGAGTCTCAGAAATCCGAGGGGACATGGGTGG 2640
Db GTGCCCCACTGCCAACCCCAAGATTAAGGAGTCTCAGAAATCCGAGGGGACATGGGTGG 8615
Qy 2641 GGATCAGAACTTCTGGGCTTGTGAGTGAGAGGGGGCCCATCTCTCTTGGTTCGAAAGGAG 2700
Db GGATCAGAACTTCTGGGCTTGTGAGTGAGAGGGGGCCCATCTCTCTTGGTTCGAAAGGAG 8675
Qy 2701 AAGAGGCTGAGGTGAATGCTTGGAGGGGAGGAATGCGGTCTGAACTCTTAATCC 2760
Db AAGAGGCTGAGGTGAATGCTTGGAGGGGAGGAATGCGGTCTGAACTCTTAATCC 8735
Qy 2761 CCAAGGAGGAGACTGTGTAAGTCCAGCTTCCGAGGTACTGACGTGGGAATGGCTGAG 2820
Db CCAAGGAGGAGACTGTGTAAGTCCAGCTTCCGAGGTACTGACGTGGGAATGGCTGAG 8795
Qy 2821 AGCTCTAAGAAATCCGCTATCCTCGGAGAGGGGCTGAAATGCTGAGGGTTGAGTTCC 2880
Db AGCTCTAAGAAATCCGCTATCCTCGGAGAGGGGCTGAAATGCTGAGGGTTGAGTTCC 8855
Qy 2881 AGGGGTTTGTAGCTCAGACTCCTTGGTGGTCCCTGGGAAGCAAGGACTGGAACCAT 2940
Db AGGGGTTTGTAGCTCAGACTCCTTGGTGGTCCCTGGGAAGCAAGGACTGGAACCAT 8915
Qy 2941 GGCTCAGGGTTGGTGTGAAGTAAATGGGATCTCTGATTTCTCAAGGGTCAAGGACT 3000
Db GGCTCAGGGTTGGTGTGAAGTAAATGGGATCTCTGATTTCTCAAGGGTCAAGGACT 8975
Qy 3001 GAGAGTTGCCATGCTTTGATCTTTCCATCTACTCTTACTCCACTTGGGGTAATCAC 3060
Db GAGAGTTGCCATGCTTTGATCTTTCCATCTACTCTTACTCCACTTGGGGTAATCAC 9035
Qy 3061 TACTCTTCTAGTCCCAAGAGTGCCTCGCGAGTATAATCTGCACATGTGCCATGTC 3120
Db TACTCTTCTAGTCCCAAGAGTGCCTCGCGAGTATAATCTGCACATGTGCCATGTC 9095
Qy 3121 CCGAGGCTGGGCGATCATCATCATTCATCAGCATCTGCGTATGCGGGGAGGCGG 3180
Db CCGAGGCTGGGCGATCATCATCATTCATCAGCATCTGCGTATGCGGGGAGGCGG 9155
Qy 3181 CGCATGAGCTCATAGTGCAGTATCCCTCGAGCGGCTCTCCGCTCAGCTCCCAA 3240
Db CGCATGAGCTCATAGTGCAGTATCCCTCGAGCGGCTCTCCGCTCAGCTCCCAA 9215
Qy 3241 CCATGAGCTGTGGACCTGGCTCCCTGTTGATGTGGCTGCTGCTGCTCCAGCCGGG 3300
Db CCATGAGCTGTGGACCTGGCTCCCTGTTGATGTGGCTGCTGCTGCTCCAGCCGGG 9275

Qy 3301 CCTGGTGTCCGATAAAGATCTTAGAACACACAGGAAACACAGGACTGAAAGGTGCTAGAGAA 3360
Db CCTGGTGTCCGATAAAGATCTTAGAACACACAGGAAACACAGGACTGAAAGGTGCTAGAGAA 9335
Qy 3361 TGGCCATATGTGCTGTCCATGAAATCTCAAGGACTTCTTGGGTGGAGGCAACAGAGCCT 3420
Db TGGCCATATGTGCTGTCCATGAAATCTCAAGGACTTCTTGGGTGGAGGCAACAGAGCCT 9395
Qy 3421 GAACTTAGGGTTTGGCCAGTCCCATGCTCTCCAAAGTGAAGTCTCCAGATAGAGGCA 3480
Db GAACTTAGGGTTTGGCCAGTCCCATGCTCTCCAAAGTGAAGTCTCCAGATAGAGGCA 9455
Qy 3481 CTGTGCCAGCATCAGCTTCACTGTACACATCTTTAAACAGGACTACCCAGGACCTG 3540
Db CTGTGCCAGCATCAGCTTCACTGTACACATCTTTAAACAGGACTACCCAGGACCTG 9515
Qy 3541 ATGAACACCATGCTGTGTGAGGAGGGGTGAAAGCATGGAAGTCTGCTGTGTGTCAGA 3600
Db ATGAACACCATGCTGTGTGAGGAGGGGTGAAAGCATGGAAGTCTGCTGTGTGTCAGA 9575
Qy 3601 GCCCAGAGGGGGCCATGACGGGTGGGAGGAGGCTGTGACTGGC 3645
Db GCCCAGAGGGGGCCATGACGGGTGGGAGGAGGCTGTGACTGGC 9620

RESULT 2
AAZ06489
ID AAZ06489 standard; DNA; 12047 BP.
XX AAZ06489;
AC AAZ06489;
XX
XX 23-NOV-1999 (first entry)
XX Human glandular kallikrein-1 (hGKL/hKLK2) promoter/enhancer region.
XX
XX prostate; cancer; drug assay; drug development; enhancer; promoter;
KW tumour; kallikrein; androgen regulation; prostate specific antigen; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT enhancer 8021..8371
FT /*tag= a
FT /note= "Enhancer activity"
XX
XX WC9941413-A2.
XX
XX PD 19-AUG-1999.
XX
XX PF 11-FEB-1999; 99WO-US003117.
XX
XX PR 12-FEB-1998; 98US-00022732.
XX
XX (CALY-) CALYDON INC.
XX
XX PI Henderson DR, Lamparski HG, Schuur ER, Yu DC;
XX
XX WPI; 1999-527378/44.
XX
XX Screening for compounds which inhibit prostate cancer using a cell line
PT containing a marker whose expression is responsive to therapeutically
PT active compounds.
XX
XX Example 6; Page 44-48; 50pp; English.
XX
XX This is the nucleotide sequence of the promoter/enhancer region of the
CC human glandular kallikrein gene (hGKL or hKLK2, encoding the hK2
CC protein). hKLK2 is a member of the kallikrein family, as is the prostate-
CC specific antigen (PSA), a chymotrypsin like protein that is synthesized
CC exclusively by normal, hyperplastic, and malignant prostatic epithelia.
CC This tissue specific nature of PSA makes it an excellent biomarker for
CC identifying benign prostatic hyperplasia (BPH) and prostatic carcinoma
CC (CaP). Elevated levels of PSA are indicative of BPH or CaP. Like PSA,

CC hKLK2 is expressed exclusively in the prostate and is up regulated by
 CC androgens, primarily by transcription activation. The proteins also
 CC exhibit a high degree of amino acid sequence identity and contain similar
 CC regulatory elements. The characterisation of genes whose expression is
 CC limited to the prostate allows the development of screening methods which
 CC can identify substances capable of specifically altering the expression
 CC of prostate-specific genes
 XX

SQ Sequence 12047 BP; 3051 A; 2484 C; 2869 G; 3643 T; 0 U; 0 Other;

Query Match 100.0%; Score 3645; DB 2; Length 12047;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCTCAATAATGTTAAGAGTGAATATGTGTCACCAAGATGAAATGTTGAGAACTA 60
 DB 5976 GGCCTCAATAATGTTAAGAGTGAATATGTGTCACCAAGATGAAATGTTGAGAACTA 6035
 QY 61 CTGTCACAGAGATTTCTCGATTTCTAGAGTGTGGGAATATAGAACTGGAGCTTGGCTT 120
 DB 6036 CTGTCACAGAGATTTCTCGATTTCTAGAGTGTGGGAATATAGAACTGGAGCTTGGCTT 6095
 QY 121 CTTTCAGCTGAATCAGAGATGAGGCTGAGTCTGAGCTTGAAGCTTGGCTTCAGAGTTGGG 180
 DB 6096 CTTTCAGCTGAATCAGAGATGAGGCTGAGTCTGAGCTTGAAGCTTGGCTTCAGAGTTGGG 6155
 QY 181 GTTGGCTTCGGAGCACATATTTGACATGTTGGGACTGTGATTTGGGGTTTGGTATTGG 240
 DB 6156 GTTGGCTTCGGAGCACATATTTGACATGTTGGGACTGTGATTTGGGGTTTGGTATTGG 6215
 QY 241 TCTGAATCTTAATGTCGTCTTGAGGCATCTAGAACTCTGAGTCTGAGATTTCT 300
 DB 6216 TCTGAATCTTAATGTCGTCTTGAGGCATCTAGAACTCTGAGTCTGAGATTTCT 6275
 QY 301 ATTATCTTGAGTAGCACATCTCCAGTCTCGTCTTCTGCTTCTAGGGCTGGAGTCTGAGT 360
 DB 6276 ATTATCTTGAGTAGCACATCTCCAGTCTCGTCTTCTGCTTCTAGGGCTGGAGTCTGAGT 6335
 QY 361 CAGTGACCGGCTCGGATTTCAATTCATATACAGTGGGCTATCTTTGGTCCATGTTT 420
 DB 6336 CAGTGACCGGCTCGGATTTCAATTCATATACAGTGGGCTATCTTTGGTCCATGTTT 6395
 QY 421 CAACCAACCAACCAATTAACCACTTAGAACCTTTCCCACTTCCCTAGCTGCAATGTAA 480
 DB 6396 CAACCAACCAACCAATTAACCACTTAGAACCTTTCCCACTTCCCTAGCTGCAATGTAA 6455
 QY 481 ACCTAGGATTTCTGTTTAAATAGGTTTCATATGAATATTTTCAGCTGATCCAACTTTACAT 540
 DB 6456 ACCTAGGATTTCTGTTTAAATAGGTTTCATATGAATATTTTCAGCTGATCCAACTTTACAT 6515
 QY 541 TCCTTTACCGTTATTTCTACACCACTTAAATGCAATCCCAATATATTCCTCGATT 600
 DB 6516 TCCTTTACCGTTATTTCTACACCACTTAAATGCAATTCCTCAATATATTCCTCGATT 6575
 QY 601 CTACCTATATAGTAAATCTCGGTTTCCAGTTTCTAGTGCATTAACATACCTGATTTA 660
 DB 6576 CTACCTATATAGTAAATCTCGGTTTCCAGTTTCTAGTGCATTAACATACCTGATTTA 6635
 QY 661 CATTTCTTTACTTTAAAGTGAATTAAGTCTCTGAGAGTTTCCAGGTTCTCAAGA 720
 DB 6636 CATTTCTTTACTTTAAAGTGAATTAAGTCTCTGAGAGTTTCCAGGTTCTCAAGA 6695
 QY 721 TGGCCCTTACTTCTGACATCAATGAGATTTCAAGGAGTTCGCCAAGATCATCTCAGGT 780
 DB 6696 TGGCCCTTACTTCTGACATCAATGAGATTTCAAGGAGTTCGCCAAGATCATCTCAGGT 6755
 QY 781 TCAGTGATGCTGTAGCTCATATTAATCAATGAAAGCTGTTATGCTCATGGCTATGG 840
 DB 6756 TCAGTGATGCTGTAGCTCATATTAATCAATGAAAGCTGTTATGCTCATGGCTATGG 6815
 QY 841 TTTATTACAGCAAAAGAAATAGAGTAAATCTAGCAAGGAAGAGTTGGATGGGGCAAA 900
 DB 6816 TTTATTACAGCAAAAGAAATAGAGTAAATCTAGCAAGGAAGAGTTGGATGGGGCAAA 6875

QY 901 GACAGGAGAGCTCCAAGTGCAGAGATTTCTGTGTTTCTCCAGTGGTGTCTATGAAA 960
 DB 5876 GACAGGAGAGCTCCAAGTGCAGAGATTTCTGTGTTTCTCCAGTGGTGTCTATGAAA 6935
 QY 961 GCAGTATCTTCTCCATACAAATGATGTGTGATAAATATTACAGTGTATGCCAATCAGGAA 1020
 DB 6936 GCAGTATCTTCTCCATACAAATGATGTGTGATAAATATTACAGTGTATGCCAATCAGGAA 6995
 QY 1021 TCACTGAGCTTGAATATATTGGAGCTTGGTTCACAGACATCTGCACACCTTTCATGG 1080
 DB 6986 TCACTGAGCTTGAATATATTGGAGCTTGGTTCACAGACATCTGCACACCTTTCATGG 7055
 QY 1081 CTGAATCTTTAGTACTTAGCCCTCCAGACGTCTACAGCTGATAGGCTGTAAACCAACAT 1140
 DB 7056 CTGAATCTTTAGTACTTAGCCCTCCAGACGTCTACAGCTGATAGGCTGTAAACCAACAT 7115
 QY 1141 GTCACCAATTAATCAGATTTAGACTATCCAGTGTGGCCCAAGCTCCGTTGAACACAG 1200
 DB 7116 GTCACCAATTAATCAGATTTAGACTATCCAGTGTGGCCCAAGCTCCGTTGAACACAG 7175
 QY 1201 GCACCTCTAAACAGGACGATATTTCAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGC 1260
 DB 7176 GCACCTCTAAACAGGACGATATTTCAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGC 7235
 QY 1261 AAAGACCTGGCTCTTTGGGCAAGAGAAATCCTTTACCGCACATCTCTTCACAGGTT 1320
 DB 7236 AAAGACCTGGCTCTTTGGGCAAGAGAAATCCTTTACCGCACATCTCTTCACAGGTT 7295
 QY 1321 ATTGTGAGATCAAAATGAGTGTGTGAGACACAGACATGCTGTGCTGTGAGA 1380
 DB 7296 ATTGTGAGATCAAAATGAGTGTGTGAGACACAGACATGCTGTGCTGTGAGA 7355
 QY 1381 GTGACTTCTATGTGTCTAACTTCTGAGTGTGAAGAGTGTAGGCAATGCTTTTTCAG 1440
 DB 7356 GTGACTTCTATGTGTCTAACTTCTGAGTGTGAAGAGTGTAGGCAATGCTTTTTCAG 7415
 QY 1441 CACTCAGAGTCTCATCTAATCTCAACATGGCTACAGGTTGGGCACTACTAGCCTC 1500
 DB 7416 CACTCAGAGTCTCATCTAATCTCAACATGGCTACAGGTTGGGCACTACTAGCCTC 7475
 QY 1501 ATTTGACAGAGAAAGGACTGTGGATGAAGAGGGGTGACCAATAGTCTCAGAGTCAATCT 1560
 DB 7476 ATTTGACAGAGAAAGGACTGTGGATGAAGAGGGGTGACCAATAGTCTCAGAGTCAATCT 7535
 QY 1561 GGATGCAAGGGGCTCCAGAGACCATGATAGACATTTGTGACAGAAATTTATGGCTGG 1620
 DB 7536 GGATGCAAGGGGCTCCAGAGACCATGATAGACATTTGTGACAGAAATTTATGGCTGG 7595
 QY 1621 ATGCTCTGCCCCGAAAGGGGATGCATTTCTTGAACCCCTTATCTCAGATCTTTCAGT 1680
 DB 7596 ATGCTCTGCCCCGAAAGGGGATGCATTTCTTGAACCCCTTATCTCAGATCTTTCAGT 7655
 QY 1681 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCGCATCATATCTCTCTGTGTC 1740
 DB 7656 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCGCATCATATCTCTCTGTGTC 7715
 QY 1741 TCTCCCTTCTCAGTCTTACTGCCCCCTTCTCCAGCTCCATCTCCAGCTGGCCAGGTG 1800
 DB 7716 TCTCCCTTCTCAGTCTTACTGCCCCCTTCTCCAGCTCCATCTCCAGCTGGCCAGGTG 7775
 QY 1801 TAGCCACAGTACCTTAATCTTTGACAGAACTATAAATGTGTATCTTACAGGGGAGAAA 1860
 DB 7776 TAGCCACAGTACCTTAATCTTTGACAGAACTATAAATGTGTATCTTACAGGGGAGAAA 7835
 QY 1861 AAAAAAGAACTCTGAAGGCTGACATTTTACGACTTGCACACACATTAAGCTTAACCTG 1920
 DB 7836 AAAAAAGAACTCTGAAGGCTGACATTTTACGACTTGCACACACATTAAGCTTAACCTG 7895
 QY 1921 CCAGTTTGTGCTGGTAGAATCTAGACTCTTGGTTCAGAGCAAAAGATTTTATTAC 1980
 DB 7896 CCAGTTTGTGCTGGTAGAATCTAGACTCTTGGTTCAGAGCAAAAGATTTTATTAC 7955

QY 1981 CCACAGCTAAGAGGCGAGCATGAACTTTGGTTTCACATTTGTTGCTTGCCTCCCAATT 2040
Db 7956 CCACAGCTAAGAGGCGAGCATGAACTTTGGTTTCACATTTGTTGCTTGCCTCCCAATT 8015
QY 2041 CATATGGGATGATCAGAGCAGTTTCAGTGGATGGACACAGGGGTTTGTGGCAAGGTGAG 2100
Db 8016 CATATGGGATGATCAGAGCAGTTTCAGTGGATGGACACAGGGGTTTGTGGCAAGGTGAG 8075
QY 2101 CAACCTTAGGCTTAGAATCTCCTCAATCTTATTAAGAGGTACTAGCAAACTTGTCCAGTCTT 2160
Db 8076 CAACCTTAGGCTTAGAATCTCCTCAATCTTATTAAGAGGTACTAGCAAACTTGTCCAGTCTT 8135
QY 2161 TGTATCTGACGGAGATATTTATTTTATTAATTTGGTTTGAAGCAGACCTCTCTGGAGGAA 2220
Db 8136 TGTATCTGACGGAGATATTTATTTTATTAATTTGGTTTGAAGCAGACCTCTCTGGAGGAA 8195
QY 2221 CATATTGTTATTTATTTGCTGAAACAGTAAACAAATCTGCTGTAATAAGACGTTAACTTT 2280
Db 8196 CATATTGTTATTTATTTGCTGAAACAGTAAACAAATCTGCTGTAATAAGACGTTAACTTT 8255
QY 2281 ATTATCTAAGCGCATGACCAACCTAGATCTGAAGCGGATACCATCTTGCAGGCTATCT 2340
Db 8256 ATTATCTAAGCGCATGACCAACCTAGATCTGAAGCGGATACCATCTTGCAGGCTATCT 8315
QY 2341 GCTGTACAAATATGCTTTGAAAGATGCTCCAGAAAAGAAAACGGTATTATTTGCTTTGCT 2400
Db 8316 GCTGTACAAATATGCTTTGAAAGATGCTCCAGAAAAGAAAACGGTATTATTTGCTTTGCT 8375
QY 2401 CAGAGACACACAGAAACATAGAGAACCATGAAAAATGTCTCCAAACACTGTTCAACC 2460
Db 8376 CAGAGACACACAGAAACATAGAGAACCATGAAAAATGTCTCCAAACACTGTTCAACC 8435
QY 2461 AGAGCCTTCACATCTTGTCTGCAGGACAGTCTTAAACATCCCATCTAGTGTGTCTACCA 2520
Db 8436 AGAGCCTTCACATCTTGTCTGCAGGACAGTCTTAAACATCCCATCTAGTGTGTCTACCA 8495
QY 2521 CATCTGGCTTCACGTCCTTAAACAGATTTCTAGTCCAGTTTCCCAACATGTTTGGCA 2580
Db 8496 CATCTGGCTTCACGTCCTTAAACAGATTTCTAGTCCAGTTTCCCAACATGTTTGGCA 8555
QY 2581 GTCCCCACATGCCAACCCACAGATAAGGGAGTCTCAGAAATCCGAGGGGACATGGTGG 2640
Db 8556 GTCCCCACATGCCAACCCACAGATAAGGGAGTCTCAGAAATCCGAGGGGACATGGTGG 8615
QY 2641 GGATCAGAACTCTTGGCTTGGTGCAGAGGGGGCCCATACTCTCTTGGTTCCGAAGGAG 2700
Db 8616 GGATCAGAACTCTTGGCTTGGTGCAGAGGGGGCCCATACTCTCTTGGTTCCGAAGGAG 8675
QY 2701 AAGAGGCTGAGGTGAATGCTCTTGGAGGGAGGAATGGGTCTCTGAATCTTAAATCC 2760
Db 8676 AAGAGGCTGAGGTGAATGCTCTTGGAGGGAGGAATGGGTCTCTGAATCTTAAATCC 8735
QY 2761 CCAAGGGAGGAGACTGTTAAGTCCCAAGCTTCCGAGTACTGACGTGGGAATGGCTGAG 2820
Db 8736 CCAAGGGAGGAGACTGTTAAGTCCCAAGCTTCCGAGTACTGACGTGGGAATGGCTGAG 8795
QY 2821 AGGTCTAAGAAATCCCGTATCCTCGGGAAGAGGGGCTGAAATTTGAGGGGTTGAGTTGC 2880
Db 8796 AGGTCTAAGAAATCCCGTATCCTCGGGAAGAGGGGCTGAAATTTGAGGGGTTGAGTTGC 8855
QY 2881 AGGGGTTTGTAGCTTGAAGTCTCTTGGTGGTCCCTGGGAAGCAAGGACTGGAACAT 2940
Db 8856 AGGGGTTTGTAGCTTGAAGTCTCTTGGTGGTCCCTGGGAAGCAAGGACTGGAACAT 8915
QY 2941 GGCTCCAGGGTTTGGTGTGAAGTAAATGGGATCTCTCTGATTTCTCAAAGGCTCAGAGGACT 3000
Db 8916 GGCTCCAGGGTTTGGTGTGAAGTAAATGGGATCTCTCTGATTTCTCAAAGGCTCAGAGGACT 8975
QY 3001 GAGAGTTGCCCATGCTTTGATCTTCCATCTACTCTTACTCCACTTGAAGTAAATCACC 3060
Db 8976 GAGAGTTGCCCATGCTTTGATCTTCCATCTACTCTTACTCCACTTGAAGTAAATCACC 9035
QY 3061 TACTCTTCTAGTTCCACAGAGTGGCGCTTCGGGAGTATAATCTGCACATGTGCCATGTC 3120

Db 9036 TACTCTTCTAGTTCCACAGAGTGGCGCTGGCGAGTATAATCTGCACATGTGCCATGTC 9095
QY 3121 CCGAGGCTGGGGCATCATCCACTCATCATTCAGCATCTGCGCTATGCGGCGGAGGCCGG 3180
Db 9096 CCGAGGCTGGGGCATCATCCACTCATCATTCAGCATCTGCGCTATGCGGCGGAGGCCGG 9155
QY 3181 GCCCATGACGTATGATGCTGAGTATCCCTCAGAGGGGCTCTCCCGTCACTGCCAA 3240
Db 9156 GCCCATGACGTATGATGCTGAGTATCCCTCAGAGGGGCTCTCCCGTCACTGCCAA 9215
QY 3241 CCATGGAGCTTGGAGCTGCGCTCCCTGGTGGATGTGGCTTGGCTGGCTGGCGCCGGGG 3300
Db 9216 CCATGGAGCTTGGAGCTGCGCTCCCTGGTGGATGTGGCTTGGCTGGCGCCGGGG 9275
QY 3301 CCTGGTGTCCGATTAAGATTCCTAGAACACAGGAAAACAGGACTGAAAGGTGCTAGAGAA 3360
Db 9276 CCTGGTGTCCGATTAAGATTCCTAGAACACAGGAAAACAGGACTGAAAGGTGCTAGAGAA 9335
QY 3361 TGGCCATATGCTGTCTCATGAAATCTCAAGGACTTCTGGGTGGAGGACACAGAGCCT 3420
Db 9336 TGGCCATATGCTGTCTCATGAAATCTCAAGGACTTCTGGGTGGAGGACACAGAGCCT 9395
QY 3421 GAACTTACGGGTTTGGCCAGTCCACTGTCTCCCAAGTGTCTCCAGATACGAGGCA 3480
Db 9396 GAACTTACGGGTTTGGCCAGTCCACTGTCTCCCAAGTGTCTCCAGATACGAGGCA 9455
QY 3481 CTGTGCCAGACAGCTTCTCATCTGACACATCTTGAACAGGGACTACCCAGGACCTG 3540
Db 9456 CTGTGCCAGACATCAGCTTCTCATCTGACACATCTTGAACAGGGACTACCCAGGACCTG 9515
QY 3541 ATGAACACCATGTTGTGTGCAGGAAGAGGGGTGAAGGCATGGACTCCTGTGTGTGTCAGA 3600
Db 9516 ATGAACACCATGTTGTGTGCAGGAAGAGGGGTGAAGGCATGGACTCCTGTGTGTGTCAGA 9575
QY 3601 GCCCAGAGGGGGCCATGACGGGTGGGAGGAGGCTGTGGACTGGC 3645
Db 9576 GCCCAGAGGGGGCCATGACGGGTGGGAGGAGGCTGTGGACTGGC 9620

RESULT 3
AAZ99934
ID AAZ99934 standard; DNA; 12047 BP.
XX AAZ99934;
AC AAZ99934;
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA sequence of comprising a human glandular kallikrein TRE.
XX
KW Glandular kallikrein; adenoviral vector; adenovirus gene;
transcriptional regulatory element; TRE; transcriptional control;
adenoviral propagation; tumour; ss.
XX
OS Homo sapiens.
XX
PN WO200015820-A1.
XX
PD 23-MAR-2000.
XX
PF 10-SEP-1999; 99WO-US020718.
XX
PR 10-SEP-1998; 98US-0099791P.
PR 09-SEP-1999; 99US-00392822.
XX
XX (CALY-) CALYDON INC.
XX Yu DC, Henderson DR;
XX WPI; 2000-271456/23.
XX
PT Adenovirus vectors comprising cell-status specific response elements
useful in gene therapy protocols for the treatment of cancers.

XX PS Disclosure; Fig 6A-H; 79pp; English.

XX CC The present sequence comprises a transcriptional regulatory element (TRE) from a human glandular kallikrein gene. The TRE is used to produce an adenoviral vector of the invention. The specification describes an adenovirus vector which comprises an adenovirus gene under transcriptional control of a cell status specific TRE. The TRE is preferably one that is essential for adenoviral propagation. The adenovirus vectors may be used for the treatment of a range of tumours such as lung, stomach, breast, colon and rectum, and uterine and cervix cancers

XX SQ Sequence 12047 BP; 3051 A; 2484 C; 2869 G; 3643 T; 0 U; 0 Other;

Query Match 100.0%; Score 3645; DB 3; Length 12047;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCCTCAATAATGTTAAAGAGTGAATGTCCTCAAGATGAAATGTTTGAGAACTA 60
Db 5976 GGCCCTCAATAATGTTAAAGAGTGAATGTCCTCAAGATGAAATGTTTGAGAACTA 6035

Qy 61 CTGTCCAGAGATTTCTCAGTCTTAGAGTGTGGGAATAGAACTCGAGCTTGGCTT 120
Db 6036 CTGTCCAGAGATTTCTCAGTCTTAGAGTGTGGGAATAGAACTCGAGCTTGGCTT 6095

Qy 121 CTTCCAGCTAGATCAGAGATGAGGCTGAAGTCTGAAGCTTGGCTTCAGCAGATTTGGG 180
Db 6096 CTTCCAGCTAGATCAGAGATGAGGCTGAAGTCTGAAGCTTGGCTTCAGCAGATTTGGG 6155

Qy 181 GTTGGCTCCGGAGCACATATTTGACATGTTGGGACTGTGAATTTGGGTTTGGTATTTC 240
Db 6156 GTTGGCTCCGGAGCACATATTTGACATGTTGGGACTGTGAATTTGGGTTTGGTATTTC 6215

Qy 241 TCTGAATCTTAATGTCCTTGAGCATCTAGATCTGAATCTGCTGAGATTTCT 300
Db 6216 TCTGAATCTTAATGTCCTTGAGCATCTAGATCTGAATCTGCTGAGATTTCT 6275

Qy 301 ATTATCTTGAGTAGGACATCTCCAGTCTCGGTTCTGCTTCTAGGGCTGGAGTCTAGT 360
Db 6276 ATTATCTTGAGTAGGACATCTCCAGTCTCGGTTCTGCTTCTAGGGCTGGAGTCTAGT 6335

Qy 361 CAGTGACCGGTCTGGCATTTCACTCATATACAGTGGGCTATCTTTGGTCCATGTTT 420
Db 6336 CAGTGACCGGTCTGGCATTTCACTCATATACAGTGGGCTATCTTTGGTCCATGTTT 6395

Qy 421 CAACCAACCAACCAACCAACCAACCACTTCCCACTTCCCTAGCTGCAATGTTAA 480
Db 6396 CAACCAACCAACCAACCAACCAACCACTTCCCACTTCCCTAGCTGCAATGTTAA 6455

Qy 481 ACCTAGGATTTCTGTTTAATAGGTTCAATAGAAATATTTTCAGCTGATCCAACTTTACAT 540
Db 6456 ACCTAGGATTTCTGTTTAATAGGTTCAATAGAAATATTTTCAGCTGATCCAACTTTACAT 6515

Qy 541 TCCTTCTACGTTATTTCTACACCACTTAAATGCAATTCCTCAATATATTCCTCGATT 600
Db 6516 TCCTTCTACGTTATTTCTACACCACTTAAATGCAATTCCTCAATATATTCCTCGATT 6075

Qy 601 CTACCTATATAGGTAATCTCGGTTTCCAGTTTCTAGTGCATTAACATACCTGATTTA 660
Db 6576 CTACCTATATAGGTAATCTCGGTTTCCAGTTTCTAGTGCATTAACATACCTGATTTA 6635

Qy 661 CATTCTTTTACTTAAAGTGGAAATAGAGTCCCTCTGGAGGTTCCAGAGTTCTCAAGA 720
Db 6636 CATTCTTTTACTTAAAGTGGAAATAGAGTCCCTCTGGAGGTTCCAGAGTTCTCAAGA 6695

Qy 721 TGGCCCTTACTTCTGACATCAATGAGATTTCAAGGAGTTCGCAAGATCATCCTCAGGT 780
Db 6696 TGGCCCTTACTTCTGACATCAATGAGATTTCAAGGAGTTCGCAAGATCATCCTCAGGT 6755

Qy 781 TCAGTGATTCGTGGTAGCCCTCATATAACTCAATGAAGCTTTATGCTCATGGCTATGG 840
Db 7836 TCAAGTGAATTCGTGGTAGCCCTCATATAACTCAATGAAGCTTTATGCTCATGGCTATGG 7895

Db 6756 TCAGTGATTCGTGGTAGCCCTCATATAACTCAATGAAGCTTTATGCTCATGGCTATGG 6815

Qy 841 TTTATTACAGCAAAAGAAATAGAGATGAAATCTAGCAAGGAGAGATTGATGGGCAAA 900

Db 6816 TTTATTACAGCAAAAGAAATAGAGATGAAATCTAGCAAGGAGAGATTGATGGGCAAA 6875

Qy 901 GACAAGGAGAGCTCCAAAGTCAGAGATTCCTGTGTTTCTCCAGTGGTGTCTATGAAA 960

Db 6876 GACAAGGAGAGCTCCAAAGTCAGAGATTCCTGTGTTTCTCCAGTGGTGTCTATGAAA 6935

Qy 961 GCAGTATCTTCTCATACAATGATGTGTATATAATTCAGTGTATTCCTCAATCAGGAA 1020

Db 6936 GCAGTATCTTCTCATACAATGATGTGTATATAATTCAGTGTATTCCTCAATCAGGAA 6995

Qy 1021 TCAACTGAGCCCTTCATTATATTGGAGCTTGGTTCACAGACATGTCACCACTTCATGG 1080

Db 6996 TCAACTGAGCCCTTCATTATATTGGAGCTTGGTTCACAGACATGTCACCACTTCATGG 7055

Qy 1081 CTGAACCTTTAGTACTTAGCCCTCCAGACGTTCTACAGCTGATAGGCTGTAAACCAACT 1140

Db 7056 CTGAACCTTTAGTACTTAGCCCTCCAGACGTTCTACAGCTGATAGGCTGTAAACCAACT 7115

Qy 1141 GTCCACCAATAATCACATGTTAGACTATCCAGTGTGGCCCAAGCTCCCTGTAAACACAG 1200

Db 7116 GTCCACCAATAATCACATGTTAGACTATCCAGTGTGGCCCAAGCTCCCTGTAAACACAG 7175

Qy 1201 GCACCTTAAACAGGACAGATATTTCAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGC 1260

Db 7176 GCACCTTAAACAGGACAGATATTTCAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGC 7235

Qy 1261 AAAAGCCTGGCTCTTTGGGCAAGAGAAATCTTTTACCGCACATCTCTCTTCACAGGTT 1320

Db 7236 AAAAGCCTGGCTCTTTGGGCAAGAGAAATCTTTTACCGCACATCTCTCTTCACAGGTT 7295

Qy 1321 ATTGTGAGATCAAAATGTTGTCATGTGTGAGACACAGACATGTCCTGGCTGTGAGA 1380

Db 7296 ATTGTGAGATCAAAATGTTGTCATGTGTGAGACACAGACATGTCCTGGCTGTGAGA 7355

Qy 1381 GTGACTTCTATGTGTCTAAATGCTGAGTGTGAGAAAGTATTAGGCAATGGCTTTTCTAG 1440

Db 7356 GTGACTTCTATGTGTCTAAATGCTGAGTGTGAGAAAGTATTAGGCAATGGCTTTTCTAG 7415

Qy 1441 CACTCAGAGATGTCATCTAATCTCAACATGCTACAGGCTGAGGCTACTCTAGGCTC 1500

Db 7416 CACTCAGAGATGTCATCTAATCTCAACATGCTACAGGCTGAGGCTACTCTAGGCTC 7475

Qy 1501 ATTTGACAGAGAAAGGACTGTGGATGAAGAGGGGTGACCAATPAGTCTCAGAGTCAATCT 1560

Db 7476 ATTTGACAGAGAAAGGACTGTGGATGAAGAGGGGTGACCAATPAGTCTCAGAGTCAATCT 7535

Qy 1561 GGATGCAAGGGCTCCAGAGACCATGATTAGACATTTCTGAGAGAAATTTATGGCTGG 1620

Db 7536 GGATGCAAGGGCTCCAGAGACCATGATTAGACATTTCTGAGAGAAATTTATGGCTGG 7595

Qy 1621 ATGCTCTGCCCCCGGAAAGGGGATGCACTTTCTTCCACCCCTATCTCAGATCTTGACT 1680

Db 7596 ATGCTCTGCCCCCGGAAAGGGGATGCACTTTCTTCCACCCCTATCTCAGATCTTGACT 7655

Qy 1681 TTGAGTTATCTCAGATCTTCTCTATGATACAGGAGCCCATCATATCTCTCTGTGTTC 1740

Db 7656 TTGAGTTATCTCAGATCTTCTCTATGATACAGGAGCCCATCATATCTCTCTGTGTTC 7715

Qy 1741 TCTCCCTTCTCAGTCTTACTGCCCCTCTTCCAGCTCCATCTCCAGTGGCCAGGTG 1800

Db 7716 TCTCCCTTCTCAGTCTTACTGCCCCTCTTCCAGCTCCATCTCCAGTGGCCAGGTG 7775

Qy 1801 TAGCCACAGTACCTAACTCTTTTTCAGAGAACTATAAATGTGTATCTCTACAGGGAGAAA 1860

Db 7776 TAGCCACAGTACCTAACTCTTTTTCAGAGAACTATAAATGTGTATCTCTACAGGGAGAAA 7835

Qy 1861 AAAAAAGAACTCTGAAAGAGCTGACATTTTACGCTTGCACCAACATAGCTAACCTG 1920

Db 7836 AAAAAAGAACTCTGAAAGAGCTGACATTTTACGCTTGCACCAACATAGCTAACCTG 7895

QY 1921 CCAGTTTGTGCTGGTGAAGTCAATGAGACTCCTGGGTGAGAGGCAAAAGATTATTTATAC 1980
Db 7896 CCAGTTTGTGCTGGTGAAGTCAATGAGACTCCTGGGTGAGAGGCAAAAGATTATTTATAC 7955
QY 1981 CCAGCTAAGAGGAGGAGTGAATTTGTTGTTTCAATTTGTTTCACTTTGCCCCCAATT 2040
Db 7956 CCAGCTAAGAGGAGGAGTGAATTTGTTGTTTCAATTTGTTTCACTTTGCCCCCAATT 8015
QY 2041 CATATGGATGATCAGAGAGTTCAGGTGATGAGACACAGGGGTTTGTGGCAAGGTGAG 2100
Db 8016 CATATGGATGATCAGAGAGTTCAGGTGATGAGACACAGGGGTTTGTGGCAAGGTGAG 8075
QY 2101 CAACCTAGGCTTGAATACTCAATCTTATAAGAGGTACTAGCAAACTTTGTCAGTCTT 2160
Db 8076 CAACCTAGGCTTGAATACTCAATCTTATAAGAGGTACTAGCAAACTTTGTCAGTCTT 8135
QY 2161 TGTATCTGACGGAGATATTTATTTATTTAATTGGTTGAAAGCAGACTACTCTGGAGGAA 2220
Db 8136 TGTATCTGACGGAGATATTTATTTAATTGGTTGAAAGCAGACTACTCTGGAGGAA 8195
QY 2221 CATATCTGATTTATTTGCTTGAACAGTAAACAACTCTGCTGTAATAGACGTTACTTT 2280
Db 8196 CATATCTGATTTATTTGCTTGAACAGTAAACAACTCTGCTGTAATAGACGTTACTTT 8255
QY 2281 ATTATCTAAGGAGTAAAGCAAACTAGATCTGAAGCGATACCATCTTGAAGGCTATCT 2340
Db 8256 ATTATCTAAGGAGTAAAGCAAACTAGATCTGAAGCGATACCATCTTGAAGGCTATCT 8315
QY 2341 GCTGTACAAATATGCTTGAAGATGCTCCAGAAAGAAACGGTATTTATTTGCTTTGCT 2400
Db 8316 GCTGTACAAATATGCTTGAAGATGCTCCAGAAAGAAACGGTATTTATTTGCTTTGCT 8375
QY 2401 CAGAAGACACAGAAACATAAGAGAACCAATGAAATTTGCTCCCAACACTGTTTCAACC 2460
Db 8376 CAGAAGACACAGAAACATAAGAGAACCAATGAAATTTGCTCCCAACACTGTTTCAACC 8435
QY 2461 AGAGCTTCCACTTCTGCTGAGGACAGTCTTAAATCCATAGTGTCTACCA 2520
Db 8436 AGAGCTTCCACTTCTGCTGAGGACAGTCTTAAATCCATAGTGTCTACCA 8495
QY 2521 CATCTGGCTTCCAGTGCCTAACCAAGATTTCTAGGTCCAGTTCCTCCACCATGTTTGGCA 2580
Db 8496 CATCTGGCTTCCAGTGCCTAACCAAGATTTCTAGGTCCAGTTCCTCCACCATGTTTGGCA 8555
QY 2581 GTGCCCCACTGCAACCCCAAGATAGGGAGTCTCAGAAATCCGAGGGGACATGGGTGG 2640
Db 8556 GTGCCCCACTGCAACCCCAAGATAGGGAGTCTCAGAAATCCGAGGGGACATGGGTGG 8615
QY 2641 GGATCAGAACTTCTGGGCTTGAAGTCCAGAGGGGGCCCTACTCTTGGTTCCGAAGGAG 2700
Db 8616 GGATCAGAACTTCTGGGCTTGAAGTCCAGAGGGGGCCCTACTCTTGGTTCCGAAGGAG 8675
QY 2701 AAGAGGCTGAGGTGAATGCTTCTGGAGGGGAGAAATGCGGTCTTGAATCTTAAATCC 2760
Db 8676 AAGAGGCTGAGGTGAATGCTTCTGGAGGGGAGAAATGCGGTCTTGAATCTTAAATCC 8735
QY 2761 CCAAGGGAGAGACTGGTAAAGTCCAGCTTCCAGGTACTGACGTGGGAAATGGCCCTGAG 2820
Db 8736 CCAAGGGAGAGACTGGTAAAGTCCAGCTTCCAGGTACTGACGTGGGAAATGGCCCTGAG 8795
QY 2821 AGGTCTAAGAAATCCCGTATCTCTCGGAAGGAGGGGCTGAAATTTGTCAGGGGTTGAGTTGC 2880
Db 8796 AGGTCTAAGAAATCCCGTATCTCTCGGAAGGAGGGGCTGAAATTTGTCAGGGGTTGAGTTGC 8855
QY 2881 AGGGTTTGTAGCTTGAAGTCTCTTGGTGGTCCCTGGGAAGCAAGGACTGGAACCAATT 2940
Db 8856 AGGGTTTGTAGCTTGAAGTCTCTTGGTGGTCCCTGGGAAGCAAGGACTGGAACCAATT 8915
QY 2941 GGCTCCAGGTTTGGTGTGAAGTAAATGGATCTCTGATTTCTCAAGGCTCAGAGGACT 3000
Db 8916 GGCTCCAGGTTTGGTGTGAAGTAAATGGATCTCTGATTTCTCAAGGCTCAGAGGACT 8975

QY 3001 GAGAGTTCGCCATGCTTTTGATCTTTCCATCTACTCTTACTCCACTTGGGGTAAATCACC 3060
Db 8976 GAGAGTTCGCCATGCTTTTGATCTTTCCATCTACTCTTACTCCACTTGGGGTAAATCACC 9035
QY 3061 TACTCTTTCTAGTTCCACAAGAGTGGCCTGCGGAGTATAATCTGSCACATGTGCCATGTC 3120
Db 9036 TACTCTTTCTAGTTCCACAAGAGTGGCCTGCGGAGTATAATCTGSCACATGTGCCATGTC 9095
QY 3121 CCGAGGCTTGGGCGATTCATCCATCATCATTCAGCATCTGCGCTATGCGGCGAGGCCGG 3180
Db 9096 CCGAGGCTTGGGCGATTCATCCACTCATCATTCAGCATCTGCGCTATGCGGCGAGGCCGG 9155
QY 3181 CGCCATGACGTTCATGCTGCGATATCCCTGCGAGCGGCTCTCCCGTCACGTCCTCAA 3240
Db 9156 CGCCATGACGTTCATGCTGCGATATCCCTGCGAGCGGCTCTCCCGTCACGTCCTCAA 9215
QY 3241 CCATGAGCTGTGAGCGTGCCTGCCCTGGTGGATGTGGCTGCTGCGTGGTGCAGGCCCGGG 3300
Db 9216 CCATGAGCTGTGAGCGTGCCTGCCCTGGTGGATGTGGCTGCTGCGTGGTGCAGGCCCGGG 9275
QY 3301 COTGGTGCCTGATAAAGATCTAGAACACAGGAAACAGGACTGAAAGGTCTAGAGAA 3360
Db 9276 COTGGTGCCTGATAAAGATCTAGAACACAGGAAACAGGACTGAAAGGTCTAGAGAA 9335
QY 3361 TGGCCATATGCTGCTGCTCCATGAAATCTCAAGGACTTCTGGGTGGAGGGCAACAGGAGCT 3420
Db 9336 TGGCCATATGCTGCTGCTCCATGAAATCTCAAGGACTTCTGGGTGGAGGGCAACAGGAGCT 9395
QY 3421 GAACTTACGGTTTGGCCAGTCCACTGCTCTCCCAAGTGTCTCCAGTGTCTCCAGTACGAGCA 3480
Db 9396 GAACTTACGGTTTGGCCAGTCCACTGCTCTCCCAAGTGTCTCCAGTGTCTCCAGTACGAGCA 9455
QY 3481 CTGTGCCAGCATCAGCTTTCATCTGTACCATCTTGTAAACAGGACTACCCAGGACCCCTG 3540
Db 9456 CTGTGCCAGCATCAGCTTTCATCTGTACCATCTTGTAAACAGGACTACCCAGGACCCCTG 9515
QY 3541 ATGAACACCATGTGTGTGTCAGGAGGGGTGAAAGCATGGACTCTCTGTGTGTGTCTGAG 3600
Db 9516 ATGAACACCATGTGTGTGTCAGGAGGGGTGAAAGCATGGACTCTCTGTGTGTGTCTGAG 9575
QY 3601 GCCCAGAGGGGGCCATGACGGGTGGGAGGAGGCTGTGGAATGGC 3645
Db 9576 GCCCAGAGGGGGCCATGACGGGTGGGAGGAGGCTGTGGAATGGC 9620

RESULT 4

AAA46852

ID AAA46852 standard; DNA; 12047 BP.

AC AAA46852;

XX

XX 03-OCT-2000 (first entry)

XX

XX Nucleotide sequence of a glandular kallikrein TRE.

XX

XX Adenoviral vector; adenoviral gene; E3 sequence; cancer;

XX target cell-specific transcriptional regulatory element; TRE;

XX selective cytotoxicity; cell growth; tumour growth; ss.

XX

XX Homo sapiens.

XX

XX WO200039319-A2.

XX

XX 06-JUL-2000.

XX

XX 30-DEC-1999; 99WO-0301249.

XX

XX 30-DEC-1998; 98US-0114262P.

XX

XX 29-DEC-1999; 99US-00474699.

XX

XX (CALY-) CALYDON INC.

XX

XX Henderson DR, Yu D;

XX DR WPI; 2000-452409/39.
XX PT New adenoviral vector for selective targeting of cancer cells, comprises
XX PT an adenovirus gene under transcriptional control of a target cell-
XX PT specific transcriptional regulatory element and an E3 sequence.
XX PS Disclosure; Fig 24; 138pp; English.
XX CC The specification describes an adenoviral vector which comprises an
XX CC adenoviral gene under the transcriptional control of a target cell-
XX CC specific transcriptional regulatory element (TRE) and an E3 sequence. The
XX CC vectors are useful for exerting selective cytotoxicity and/or suppressing
XX CC cell growth (including tumour growth). This is especially useful in
XX CC treating cancer in which targeted cell killing is desirable. This is also
XX CC useful for targeted cytotoxic effects in other, non-tumour cells, when
XX CC selective destruction and/or suppression of these cells is desirable. The
XX CC vectors can also be useful for detecting the presence of cells which
XX CC permit function of a target cell-specific TRE in, for example, an
XX CC appropriate biological (such as clinical) sample. The adenovirus
XX CC vector(s) can optionally selectively produce one or more proteins of
XX CC interest in a target cell by using a heterologous, i.e., non-adenoviral,
XX CC TRE. The present sequence represents a human glandular kallikrein TRE,
XX CC which is used in the course of the invention
XX CC
SQ Sequence 12047 BP; 3051 A; 2484 C; 2869 G; 3643 T; 0 U; 0 Other;
Query Match 100.0%; Score 3645; DB 3; Length 12047;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCCCTCAATAATGTTAAAGAGTGTAAATGTGTCCTCAAGAGTGAATAATGTTGAGAACTA 60
DB 5976 GGCCCTCAATAATGTTAAAGAGTGTAAATGTGTCCTCAAGAGTGAATAATGTTGAGAACTA 6035
QY 61 CTGTCCAGAGATTTCTCGAGTCTAGAGTGGGATATAGAACTGGAGCTTGGCTT 120
DB 6036 CTGTCCAGAGATTTCTCGAGTCTAGAGTGGGATATAGAACTGGAGCTTGGCTT 6095
QY 121 CTTCCAGCTAGATCAGAGATGATGGGCTGAAGTCTGAAGCTTGGCTTCCAGAGTGTGGG 180
DB 6096 CTTCCAGCTAGATCAGAGATGATGGGCTGAAGTCTGAAGCTTGGCTTCCAGAGTGTGGG 6155
QY 181 GTTGGCTCCGGAGCACAATATTTGACATGTTGGGATCTGTGATTTGGGTTTGTATTTCG 240
DB 6156 GTTGGCTCCGGAGCACAATATTTGACATGTTGGGATCTGTGATTTGGGTTTGTATTTCG 6215
QY 241 TCTGAATCCTTAATGTCGTCTGAGGCATCTAGAACTCTGAGTCTGAGTCTGAGTCTGAGT 300
DB 6216 TCTGAATCCTTAATGTCGTCTGAGGCATCTAGAACTCTGAGTCTGAGTCTGAGTCTGAGT 6275
QY 301 ATTATCTTGAGTAGGACATCTCCAGTCTCGGTTCTGCTTCTAGGGCTGGAGTCTGTAGT 360
DB 6276 ATTATCTTGAGTAGGACATCTCCAGTCTCGGTTCTGCTTCTAGGGCTGGAGTCTGTAGT 6335
QY 361 CAGTGACCCGCTCGGATTTCACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 420
DB 6336 CAGTGACCCGCTCGGATTTCACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 6395
QY 421 CAACCAACCAACCAACCAATAGAACCTTTTCCCACTTCCCTAGCTGCAATGTTAA 480
DB 6396 CAACCAACCAACCAACCAATAGAACCTTTTCCCACTTCCCTAGCTGCAATGTTAA 6455
QY 481 ACCTAGGATTTCTTTAAATAGGTTTCAATGAATATTTTCAGCTGATCCAACTTTACAT 540
DB 6456 ACCTAGGATTTCTTTAAATAGGTTTCAATGAATATTTTCAGCTGATCCAACTTTACAT 6515
QY 541 TCCTTCTACCGTTATTTCTACACCCACCTTAAATGCAATTTCCCAATATATTTCCCTGGATT 600
DB 6516 TCCTTCTACCGTTATTTCTACACCCACCTTAAATGCAATTTCCCAATATATTTCCCTGGATT 6575
QY 601 CTACCTATATATGTAATCTCGGCTTTGCCAGTTTCTAGTGCATTAACATACCTGATTAA 660
DB 6601 CTACCTATATATGTAATCTCGGCTTTGCCAGTTTCTAGTGCATTAACATACCTGATTAA 6660

DB 6576 CTACCTATATATGTAATCTCGGCTTTGCCAGTTTCTAGTGCATTAACATACCTGATTAA 6635
QY 661 CATTTCTTTTAAAGTGAATAAGAGTCCCTCTGCGAGAGTTTCAGGAGTTCTCAAGA 720
DB 6636 CATTTCTTTTAAAGTGAATAAGAGTCCCTCTGCGAGAGTTTCAGGAGTTCTCAAGA 6695
QY 721 TGGCCCTTACTCTGACATCAATTTGAGATTTCAAGGGAGTTCGCAAGATCATCTCAGGT 780
DB 6696 TGGCCCTTACTCTGACATCAATTTGAGATTTCAAGGGAGTTCGCAAGATCATCTCAGGT 6755
QY 781 TCAGTGATGCTGTAGCCCTCATATTAATCAATGAAGCTGTTATGCTCATGCTATGG 840
DB 6756 TCAGTGATGCTGTAGCCCTCATATTAATCAATGAAGCTGTTATGCTCATGCTATGG 6815
QY 841 TTTTATTACAGCAAAAGAAATAGAGATGAATAATCTAGCAAGGAGAGTTGCATGGGCAAA 900
DB 6816 TTTTATTACAGCAAAAGAAATAGAGATGAATAATCTAGCAAGGAGAGTTGCATGGGCAAA 6875
QY 901 GACAAGGAGAGCTCCAAAGTCAGAGATTCCTGTTGTTTCTCCAGTGGTGTATGAAA 960
DB 6876 GACAAGGAGAGCTCCAAAGTCAGAGATTCCTGTTGTTTCTCCAGTGGTGTATGAAA 6935
QY 961 GCAGTATCTTCTCCATCAATGATGCTGATATATTCAGTGTATTCGCAATCAGGGAAC 1020
DB 6936 GCAGTATCTTCTCCATCAATGATGCTGATATATTCAGTGTATTCGCAATCAGGGAAC 6995
QY 1021 TCAACTGAGCCTTGATTATATTTGAGGCTTGGTTGTCACAGACATGTCACCACTTCATGG 1080
DB 6996 TCAACTGAGCCTTGATTATATTTGAGGCTTGGTTGTCACAGACATGTCACCACTTCATGG 7055
QY 1081 CTGAACCTTTAGTACTTAGCCCTCCAGAGCTTCACAGCTGATAGGCTGTAACCCACATT 1140
DB 7056 CTGAACCTTTAGTACTTAGCCCTCCAGAGCTTCACAGCTGATAGGCTGTAACCCACATT 7115
QY 1141 GTCCACCAATCAATTTGTTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 1200
DB 7116 GTCCACCAATCAATTTGTTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 7175
QY 1201 GCATCTTAAACAGGAGAGATTTTAAAGCTTTAGAGTACATCCCCAGAGAGTGAATGC 1260
DB 7176 GCATCTTAAACAGGAGAGATTTTAAAGCTTTAGAGTACATCCCCAGAGAGTGAATGC 7235
QY 1261 AAAGACCTGGGCTCTTTGGGCAAGGAGATTCCTTTACCGACACATCTCTCTTCACAGGTT 1320
DB 7236 AAAGACCTGGGCTCTTTGGGCAAGGAGATTCCTTTACCGACACATCTCTCTTCACAGGTT 7295
QY 1321 ATTGTGAGGATCAAAATGTTGTCATGTGTGAGACACAGACATGTCGTGGTGTGAGA 1380
DB 7296 ATTGTGAGGATCAAAATGTTGTCATGTGTGAGACACAGACATGTCGTGGTGTGAGA 7355
QY 1381 GTGACTTCTATGCTGTCTTAACTTGAAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGT 1440
DB 7356 GTGACTTCTATGCTGTCTTAACTTGAAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGT 7415
QY 1441 CACTCACAGATGCTCATCTAATCTCCACATGGCTACAGGTTGGGAGTGTAGGCTC 1500
DB 7416 CACTCACAGATGCTCATCTAATCTCCACATGGCTACAGGTTGGGAGTGTAGGCTC 7475
QY 1501 ATTTGACAGAGAAAGGAGTGTGATTAAGGAGGAGTGAAGGAGTGAAGGAGTGAAGT 1560
DB 7476 ATTTGACAGAGAAAGGAGTGTGATTAAGGAGGAGTGAAGGAGTGAAGGAGTGAAGT 7535
QY 1561 GGATGCAAGGGGCTCCAGAGGACCATGATTAGACATTTGTCGAGAGAAATTTATGGCTGG 1620
DB 7536 GGATGCAAGGGGCTCCAGAGGACCATGATTAGACATTTGTCGAGAGAAATTTATGGCTGG 7595
QY 1621 ATGCTCTGCCCCGAAAGGGGATGACATTTCTTGACCCCTTCTCTCAGATCTTGACT 1680
DB 7596 ATGCTCTGCCCCGAAAGGGGATGACATTTCTTGACCCCTTCTCTCAGATCTTGACT 7655
QY 1681 TTGAGGTTTATCTCAGATTTCTCTATGATACAGAGGAGCCATCAATAATCTCTGTGTCC 1740
DB 7656 TTGAGGTTTATCTCAGATTTCTCTATGATACAGAGGAGCCATCAATAATCTCTGTGTCC 7715

QY 1741 TCTCCCTTCTCAGTCTTACTGCCCACTCTTCCAGCTCCATCTCCAGTGGCCAGGTG 1800
Db 7716 TCTCCCTTCTCAGTCTTACTGCCCACTCTTCCAGCTCCATCTCCAGTGGCCAGGTG 7775
QY 1801 TAGCCAGTACCTAACTCTTTTCAGAGAACTATAAATGTATCTCTACAGGGGAGAAA 1860
Db 7776 TAGCCAGTACCTAACTCTTTTCAGAGAACTATAAATGTATCTCTACAGGGGAGAAA 7835
QY 1861 AAAAAAGAACTCTGAAAGAGCTGACATTTTACCGACTTGGCAACACATAAGCTAACCTG 1920
Db 7836 AAAAAAGAACTCTGAAAGAGCTGACATTTTACCGACTTGGCAACACATAAGCTAACCTG 7895
QY 1921 CCAAGTTTGTGCTGTAGAACTCATGAGACTCTCGGTGAGAGGCAAGAAATTTATTAC 1980
Db 7896 CCAAGTTTGTGCTGTAGAACTCATGAGACTCTCGGTGAGAGGCAAGAAATTTATTAC 7955
QY 1981 CCAAGTTTGTGCTGTAGAACTCATGAGACTCTCGGTGAGAGGCAAGAAATTTATTAC 2040
Db 7956 CCAAGTTTGTGCTGTAGAACTCATGAGACTCTCGGTGAGAGGCAAGAAATTTATTAC 8015
QY 2041 CATATGGATGATCAGAGAGTTTCAAGTGGATGACACAGGGGTTTGGCAAGGTGAG 2100
Db 8016 CATATGGATGATCAGAGAGTTTCAAGTGGATGACACAGGGGTTTGGCAAGGTGAG 8075
QY 2101 CAACCTAGGCTTAGAAATCCTCAATCTTATAAGAGGTACTAGCAAACTTGTCCAGTCTT 2160
Db 8076 CAACCTAGGCTTAGAAATCCTCAATCTTATAAGAGGTACTAGCAAACTTGTCCAGTCTT 8135
QY 2161 TGTATCTGAGGAGATTTATCTTTTATATTTGGTTTGAAGAGAGCTACTCTGAGGAA 2220
Db 8136 TGTATCTGAGGAGATTTATCTTTTATATTTGGTTTGAAGAGAGCTACTCTGAGGAA 8195
QY 2221 CATATTGTTATTGTCTGAAACAGTAAACAAATCTGCTGTAAATAGACGTTAACTTT 2280
Db 8196 CATATTGTTATTGTCTGAAACAGTAAACAAATCTGCTGTAAATAGACGTTAACTTT 8255
QY 2281 ATTATCTAGGAGTAAAGCAACTAGATCTGAAGCGGATACCATCTTCCAGAGGTATCT 2340
Db 8256 ATTATCTAGGAGTAAAGCAACTAGATCTGAAGCGGATACCATCTTCCAGAGGTATCT 8315
QY 2341 GCTGTCAAAATATGCTTGAAGATGGTCCAGAAAAGAAACGGTATTATTCCTTTGCT 2400
Db 8316 GCTGTCAAAATATGCTTGAAGATGGTCCAGAAAAGAAACGGTATTATTCCTTTGCT 8375
QY 2401 CAGAAGACACAGAAACATAGAGAACCATGGAAATTTGTCTCCAAACACTGTTCAACC 2460
Db 8376 CAGAAGACACAGAAACATAGAGAACCATGGAAATTTGTCTCCAAACACTGTTCAACC 8435
QY 2461 AGAGCCTTCCACTCTTGTCTGAGGACAGTCTTAACATCCCATCTAGTGTCTACCA 2520
Db 8436 AGAGCCTTCCACTCTTGTCTGAGGACAGTCTTAACATCCCATCTAGTGTCTACCA 8495
QY 2521 CATCTGGCTTCAACGCTTAAACCAAGATTTCTAGGTCCAGTTTCCCACTGTTGGCA 2580
Db 8496 CATCTGGCTTCAACGCTTAAACCAAGATTTCTAGGTCCAGTTTCCCACTGTTGGCA 8555
QY 2581 GTCCCCCACTGCCAACCCAGAAATAGAGGAGTGTCTAGAAATTCGAGGGGACATGGGTGG 2640
Db 8556 GTCCCCCACTGCCAACCCAGAAATAGAGGAGTGTCTAGAAATTCGAGGGGACATGGGTGG 8615
QY 2641 GGATCAGAACTTCTGGGCTTGTAGTGCAGAGGGGGCCCATCTCTTGGTTCCGAGAGAGG 2700
Db 8616 GGATCAGAACTTCTGGGCTTGTAGTGCAGAGGGGGCCCATCTCTTGGTTCCGAGAGAGG 8675
QY 2701 AAGAGGCTGAGGTGAATGTCTTTGAGGGAGGAATGTGGGTTCTGAACTCTTTAAATCC 2760
Db 8676 AAGAGGCTGAGGTGAATGTCTTTGAGGGAGGAATGTGGGTTCTGAACTCTTTAAATCC 8735
QY 2761 CCAAGGAGGAGACTGTGAAGTCCAGCTTCCGAGGTACTGACGTGGGAATGGCTGAG 2820
Db 8736 CCAAGGAGGAGACTGTGAAGTCCAGCTTCCGAGGTACTGACGTGGGAATGGCTGAG 8795

QY 2821 AGGTCTAAGAAATCCGATATCTCCGGAGAGGGGGCTGAATTTGTAGGGTTGAGTTGC 2880
Db 8796 AGGTCTAAGAAATCCGATATCTCCGGAGAGGGGGCTGAATTTGTAGGGTTGAGTTGC 8855
QY 2881 AGGGTTTGTAGTTTGTAGACTCTCTTGGTGGGTCCCTGGGAAGCAAGACTGGGAACCAT 2940
Db 8856 AGGGTTTGTAGTTTGTAGACTCTCTTGGTGGGTCCCTGGGAAGCAAGACTGGGAACCAT 8915
QY 2941 GGCTCCAGGTTTGGTGTGAAGGTAAATGGGATCTCTCTGATTTCTCAAAGGTCAGAGACT 3000
Db 8916 GGCTCCAGGTTTGGTGTGAAGGTAAATGGGATCTCTCTGATTTCTCAAAGGTCAGAGACT 8975
QY 3001 GAGAGTTGCCCATCTGTTGATCTTCCATCTTACTCTTACTCTTACTCTTACTCTTACTCT 3060
Db 8976 GAGAGTTGCCCATCTGTTGATCTTCCATCTTACTCTTACTCTTACTCTTACTCTTACTCT 9035
QY 3061 TACTCTTCTAGTTTCCCAAGAGTGGCTGGCGAGATATAATCTGCAATCTGCAATCTGTC 3120
Db 9036 TACTCTTCTAGTTTCCCAAGAGTGGCTGGCGAGATATAATCTGCAATCTGCAATCTGTC 9095
QY 3121 CCGAGGCTGGGATCATCCACTCATCTTACACTCTGCGCTATCGGCTATCGGCGAGGCGG 3180
Db 9096 CCGAGGCTGGGATCATCCACTCATCTTACACTCTGCGCTATCGGCTATCGGCGAGGCGG 9155
QY 3181 CGCCATGACGTCATGTAGTCCGACTATCCCTGAGCGCGCTCTCCCGTCACTGCCAA 3240
Db 9156 CGCCATGACGTCATGTAGTCCGACTATCCCTGAGCGCGCTCTCCCGTCACTGCCAA 9215
QY 3241 CCATGGAGCTGTGACGCTGGTCCCTGGTGGATGTGGCTGGTGGTGGTGGTGGTGGTGG 3300
Db 9216 CCATGGAGCTGTGACGCTGGTCCCTGGTGGATGTGGCTGGTGGTGGTGGTGGTGGTGG 9275
QY 3301 CCTGGTCTCCATATAAGATCTTAGAACCAACAGGAAACAGGACTGAAAGTGTCTAGAGAA 3360
Db 9276 CCTGGTCTCCATATAAGATCTTAGAACCAACAGGAAACAGGACTGAAAGTGTCTAGAGAA 9335
QY 3361 TGGCCATATGTCTGTCTTCCATGAAATCTCAAGGACTTCTGGTGGAGGACACAGGCTCT 3420
Db 9336 TGGCCATATGTCTGTCTTCCATGAAATCTCAAGGACTTCTGGTGGAGGACACAGGCTCT 9395
QY 3421 GAACTTACGGGTTTGGCCAGTCCACTGTCTCCCAAGTGTCTCCAGATACGAGGCA 3480
Db 9396 GAACTTACGGGTTTGGCCAGTCCACTGTCTCCCAAGTGTCTCCAGATACGAGGCA 9455
QY 3481 CTGTGCCAGCATCAGCTTCTGTACACATCTTGTAAACAGGACTACCCAGGACCTGT 3540
Db 9456 CTGTGCCAGCATCAGCTTCTGTACACATCTTGTAAACAGGACTACCCAGGACCTGT 9515
QY 3541 ATGAACCCATGTGTGTGAGGAGAGGGGGTCAAGGSCATGGACTCTGTGTGTGTGTGTGT 3600
Db 9516 ATGAACCCATGTGTGTGAGGAGAGGGGGTCAAGGSCATGGACTCTGTGTGTGTGTGTGT 9575
QY 3601 GCCCAGAGGGGGCCATGACGGGTGGGAGGAGGCTGTGGACTGGC 3645
Db 9576 GCCCAGAGGGGGCCATGACGGGTGGGAGGAGGCTGTGGACTGGC 9620

RESULT 5

AAH43617
ID AAH43617 standard; cDNA; 12047 BP.

XX
AC AAH43617;

XX
DT 07-JAN-2002 (first entry)

XX
DE Human glandular kallikrein-TRE.

XX
KW Adenovirus; ADP; replication-competent; adenoviral vector; TRE; PCR;
transcriptional regulatory element; mutation; deletion; IRIS; primer;
promoter; internal ribosome entry site; cytotoxic; cancer; bladder;
amplify; polymerase chain reaction; alpha-fetoprotein; AFP; EMCV;
encephalomyocarditis virus; vascular endothelial growth factor; VEGF;
immunoglobulin heavy-chain binding protein; BIP; uroplakin II; PDGF;

Db 7356 GTGACTTCTATGTGTGCTAAACATTTGCTGAGTGCTAAGAAAGTATTAGGCATGCTTTTCAG 7415
Qy 1441 CACTCAGAGATGCTCATCTAATCCTCACACATGGCTACAGGGTGGGCACTACTAGCCTC 1500
Db 7416 CACTCAGAGATGCTCATCTAATCCTCACACATGGCTACAGGGTGGGCACTACTAGCCTC 7475
Qy 1501 ATTTCAGAGAGAAAGGACTGTGATAGAGAGGGGTGACCAATAGGTGAGAGTCAATCTT 1560
Db 7476 ATTTCAGAGAGAAAGGACTGTGATAGAGAGGGGTGACCAATAGGTGAGAGTCAATCTT 7535
Qy 1561 GGATGCAAGGGGCTCCAGAGAGACCATGATTAGACATTTGCTGAGAGAAATATGCTCG 1620
Db 7536 GGATGCAAGGGGCTCCAGAGAGACCATGATTAGACATTTGCTGAGAGAAATATGCTCG 7595
Qy 1621 ATGTCTCTGCCCGGAAAGGGGATGCACTTTCTTTGACCCCTATCTCAGATCTTTGACT 1680
Db 7596 ATGTCTCTGCCCGGAAAGGGGATGCACTTTCTTTGACCCCTATCTCAGATCTTTGACT 7655
Qy 1681 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCCCATCATATATCTCTGTGTCC 1740
Db 7656 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCCCATCATATATCTCTGTGTCC 7715
Qy 1741 TCTCCCTCTCTCAGTCTTACTGCCCACTCTTCCAGCTCCATCTCCAGCTGCCAGGTG 1800
Db 7716 TCTCCCTCTCTCAGTCTTACTGCCCACTCTTCCAGCTCCATCTCCAGCTGCCAGGTG 7775
Qy 1801 TAGCCAGATACCTAATCTTTGAGAGAACTATAAATGTGTATCTCAGAGGGAGAAAA 1860
Db 7776 TAGCCAGATACCTAATCTTTGAGAGAACTATAAATGTGTATCTCAGAGGGAGAAAA 7835
Qy 1861 AAAAAAGAACTCTGAAAGAGCTGACATTTTACCGACTTGCAAAACACATAAGCTAACCTG 1920
Db 7836 AAAAAAGAACTCTGAAAGAGCTGACATTTTACCGACTTGCAAAACACATAAGCTAACCTG 7895
Qy 1921 CCGAGTTTGTGCTGAGTAACTCATGAGACTCTGGGTGAGAGGCAAAAGATTTATTAC 1980
Db 7896 CCGAGTTTGTGCTGAGTAACTCATGAGACTCTGGGTGAGAGGCAAAAGATTTATTAC 7955
Qy 1981 CCACAGTAAGGAGGAGCAGTAACCTTTGTGTTACATTTGTTACCTTTGCCCCCAATT 2040
Db 7956 CCACAGTAAGGAGGAGCAGTAACCTTTGTGTTACATTTGTTACCTTTGCCCCCAATT 8015
Qy 2041 CATATGGATGATCAGAGCAGTTCAAGTGGATGGAACACAGGGGTTTGTGGCAAGGTGAG 2100
Db 8016 CATATGGATGATCAGAGCAGTTCAAGTGGATGGAACACAGGGGTTTGTGGCAAGGTGAG 8075
Qy 2101 CAACCTAGGCTTAGAATCTCCTAATCTTATAGAGGTACTAGCAACTTGTCCAGTCTT 2160
Db 8076 CAACCTAGGCTTAGAATCTCCTAATCTTATAGAGGTACTAGCAACTTGTCCAGTCTT 8135
Qy 2161 TGTATCTGACGGAGATATTATCTTTATATTTGGTTGAAAGCAGACCTACTCTGGAGGAA 2220
Db 8136 TGTATCTGACGGAGATATTATCTTTATATTTGGTTGAAAGCAGACCTACTCTGGAGGAA 8195
Qy 2221 CATATTGATTTATTTGCTGAGCAGTAACAAATCTGCTGTAATAATAGACGTTAACTTT 2280
Db 8196 CATATTGATTTATTTGCTGAGCAGTAACAAATCTGCTGTAATAATAGACGTTAACTTT 8255
Qy 2281 ATTATCTAAGGAGTAAGCAAACTAGATCTGAAGCGATACCATCTTGCAAGGCTATCT 2340
Db 8256 ATTATCTAAGGAGTAAGCAAACTAGATCTGAAGCGATACCATCTTGCAAGGCTATCT 8315
Qy 2341 GCTGTCAAAATATGCTTTGAAAGATGCTCCAGAAAAAGAAACGGTATTTATGCTTTGCT 2400
Db 8316 GCTGTCAAAATATGCTTTGAAAGATGCTCCAGAAAAAGAAACGGTATTTATGCTTTGCT 8375
Qy 2401 CAGAAGACACAGAAACATAAGAGAACCATGGAATAATGTCCTCCAAACACTGTTCAACC 2460
Db 8376 CAGAAGACACAGAAACATAAGAGAACCATGGAATAATGTCCTCCAAACACTGTTCAACC 8435
Qy 2461 AGAGCCTTCACCTCTGCTGACAGGACAGTCTTAAACATCCCATCATTAGTGTGTACCA 2520
Db 8436 AGAGCCTTCACCTCTGCTGACAGGACAGTCTTAAACATCCCATCATTAGTGTGTACCA 8495

Qy 2521 CATCTGGCTTCAACCGTGCCTAACCAAGATTTCTAGTCCAGTTCCTCCACCATGTTTGCA 2580
Db 8496 CATCTGGCTTCAACCGTGCCTAACCAAGATTTCTAGTCCAGTTCCTCCACCATGTTTGCA 8555
Qy 2581 GTGCCCACTGCCAACCCAGAAATAAGGAGTGTCTCAGAAATCCGAGGGGACATGGGTGG 2640
Db 8556 GTGCCCACTGCCAACCCAGAAATAAGGAGTGTCTCAGAAATCCGAGGGGACATGGGTGG 8615
Qy 2641 GGATCAGAAATCTCTGGGCTTGAGTGCAGAGGGGGCCCATACTCTCTGTTGTTCCGAAGGAGG 2700
Db 8616 GGATCAGAAATCTCTGGGCTTGAGTGCAGAGGGGGCCCATACTCTCTGTTCCGAAGGAGG 8675
Qy 2701 AAGAGCTTGAAGGTGAATGTCTTTGAGGGGAGAAATGTGGGTTCTGAACTCTTAAATCC 2760
Db 8676 AAGAGCTTGAAGGTGAATGTCTTTGAGGGGAGAAATGTGGGTTCTGAACTCTTAAATCC 8735
Qy 2761 CCAAGGGAGGAGACTGTTAAGGTCCAGCTTCCAGAGTACTGACGTGGGAAATGGCTGAG 2820
Db 8736 CCAAGGGAGGAGACTGTTAAGGTCCAGCTTCCAGAGTACTGACGTGGGAAATGGCTGAG 8795
Qy 2821 AGGCTAAGAAATCCCGTATCTCCGGAAAGGAGGGGTGAAATTTGTAGGGGTTGAGTTGC 2880
Db 8796 AGGCTAAGAAATCCCGTATCTCCGGAAAGGAGGGGTGAAATTTGTAGGGGTTGAGTTGC 8855
Qy 2881 AGGGTTTGTAGCTTGAGACTCTCTGTTGGTCCCTGGGAGCAAGACTTGGAAACCAAT 2940
Db 8856 AGGGTTTGTAGCTTGAGACTCTCTGTTGGTCCCTGGGAGCAAGACTTGGAAACCAAT 8915
Qy 2941 GGCTCCAGGGTTTGTGTGAAGGTAATGGGATCTCTGATTTCTCAAAGGGTCAGAGGACT 3000
Db 8916 GGCTCCAGGGTTTGTGTGAAGGTAATGGGATCTCTGATTTCTCAAAGGGTCAGAGGACT 8975
Qy 3001 GAGAGTTGCCATGCTTTGATCTTTCCATCTACTCTCTTACTCCACTTGAGGGTAAATCACC 3060
Db 8976 GAGAGTTGCCATGCTTTGATCTTTCCATCTACTCTCTTACTCCACTTGAGGGTAAATCACC 9035
Qy 3061 TACTCTTCTAGTTCCACAAGAGTGGCTGCGCAGTATAATCTGCACATGTGCCATGTC 3120
Db 9036 TACTCTTCTAGTTCCACAAGAGTGGCTGCGCAGTATAATCTGCACATGTGCCATGTC 9095
Qy 3121 CCGAGGCTGGGGCANTATCCACTCATCTATTCAGATCTGCGCTATGCGGCGAGGCGCG 3180
Db 9096 CCGAGGCTGGGGCANTATCCACTCATCTATTCAGATCTGCGCTATGCGGCGAGGCGCG 9155
Qy 3181 CGCCATGACGTCATGATGCTAGCTGCGACTCTCCGTCAGCGCGCTCTCCGTCACGTCCTCAA 3240
Db 9156 CGCCATGACGTCATGATGCTAGCTGCGACTCTCCGTCAGCGCGCTCTCCGTCACGTCCTCAA 9215
Qy 3241 CCATGGAGCTTGGACGTCGTCCTCCCTGGTGGATGTGGCTGTGCTGCTGCTGCTGCTGCTG 3300
Db 9216 CCATGGAGCTTGGACGTCGTCCTCCCTGGTGGATGTGGCTGTGCTGCTGCTGCTGCTGCTG 9275
Qy 3301 CCTGGTGTCCGATTAAGATCCTAGAACACAGGAAACAGGACTGAAAGGTGCTTAGAGAA 3360
Db 9276 CCTGGTGTCCGATTAAGATCCTAGAACACAGGAAACAGGACTGAAAGGTGCTTAGAGAA 9335
Qy 3361 TGGCCATATGCTGCTGCTCCATGAAATCTCAAGGACTTCTTGGGTGGAGGCAACAGAGCCT 3420
Db 9336 TGGCCATATGCTGCTGCTCCATGAAATCTCAAGGACTTCTTGGGTGGAGGCAACAGAGCCT 9395
Qy 3421 GAACTTAGGGTTTGGCCAGTCCACTGTCTCCCAAGTGTCTCCCAAGTGTCTCCCAAGTGTCT 3480
Db 9396 GAACTTAGGGTTTGGCCAGTCCACTGTCTCCCAAGTGTCTCCCAAGTGTCTCCCAAGTGTCT 9455
Qy 3481 CTGTGCCAGCATCAGCTTCTGTACCAATCTTGTAAACAGGACTACCCAGGACCCCTG 3540
Db 9456 CTGTGCCAGCATCAGCTTCTGTACCAATCTTGTAAACAGGACTACCCAGGACCCCTG 9515
Qy 3541 ATGAACACCATGGTGTGTGACAGGAGGGGTGAAGGCAATGGACTCTGTGTGTGTGCTAGA 3600
Db 9516 ATGAACACCATGGTGTGTGACAGGAGGGGTGAAGGCAATGGACTCTGTGTGTGTGCTAGA 9575

QY 3601 GCCCAGAGGGGCCATGACGGGTGGGAGGAGGCTGTGGACTGGC 3645
DB 9576 GCCCAGAGGGGCCATGACGGGTGGGAGGAGGCTGTGGACTGGC 9620

RESULT 6
AAF87248
ID AAF87248 standard; DNA; 12047 BP.
XX
AC AAF87248;
XX
DT 26-MAR-2002 (first entry)
DE Human glandular kallikrein-TRE coding sequence.
XX
KW Tumour growth suppression; adenovirus vector; antineoplastic agent;
KW transcriptional regulatory element; TRE; radiotherapy; bladder cancer;
KW prostate cancer; liver cancer; breast cancer; colon cancer; melanoma;
KW ovarian cancer; pancreatic cancer; lung cancer; brain cancer; therapy;
KW glandular kallikrein-TRE; ds.
XX
OS Homo sapiens.
XX
XX WO200172341-A2.
XX
PD 04-OCT-2001.
XX
PF 21-MAR-2001; 2001WO-US009042.
XX
PR 24-MAR-2000; 2000US-0192015P.
XX
XX (CALY-) CALYDON INC.
XX
PI Yu D, Chen Y, Henderson DR;
XX
DR WPI; 2001-648426/74.
XX
PT Suppression of tumor growth, e.g. liver, bladder or breast cancer,
PT comprises using a synergistic combination of adenovirus vector and
PT antineoplastic agent or radiotherapy.
XX
PS Disclosure; Page 174-181; 248pp; English.
XX
CC This sequence is a human glandular kallikrein-TRE coding sequence used in
CC the scope of the invention. The invention relates to a method for the
CC suppression of tumour growth comprising the administration of: (a) a
CC target cell-specific adenovirus vector comprising an adenoviral gene
CC essential for replication under transcriptional control of a target cell-
CC specific transcriptional regulatory element (TRE); and (b) at least one
CC antineoplastic agent; or (c) a course of radiotherapy where the amount of
CC (a) and/or (b) or (c) is lower than that known to be effective for
CC suppressing tumour growth when administered alone. The method is used for
CC suppression of tumour growth for treatment of e.g. bladder cancer,
CC prostate cancer, liver cancer, breast cancer, colon cancer, melanoma,
CC ovarian cancer, pancreatic cancer, lung cancer or brain cancer. The
CC combinations enhance the efficacy of treatment, allowing lower doses to
CC be administered, reducing toxicity and suffering of the patient
XX
SQ Sequence 12047 BP; 3051 A; 2484 C; 2869 G; 3643 T; 0 U; 0 Other;

Query Match 100.0%; Score 3645; DB 5; Length 12047;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCCTCAATAATGTTAAGAGTGTAATGTCGTCGCAAGATGAAATGTTTGAGAACTA 60
DB 5976 GGCCCTCAATAATGTTAAGAGTGTAATGTCGTCGCAAGATGAAATGTTTGAGAACTA 6035

QY 61 CTGTCCAGAGATTTTCCTGAGTTCTAGAGTGTGGGAAATATAGAACTCGAGCTTGGCTT 120
DB 6036 CTGTCCAGAGATTTTCCTGAGTTCTAGAGTGTGGGAAATATAGAACTCGAGCTTGGCTT 6095

QY 121 CTTGAGCCTAGATCAGGAGTATGGGCTCAAGTCTGAAGCTTGGCTTCAGCAGTTGGG 180

DB 6096 CTTGAGCCTAGATCAGGAGTATGGGCTGAAGTCTGAAGCTTGGCTTCAGCAGTTGGG 6155
QY 181 GTTGGCTTCGGAGCACATATTTGACATGTTGGACTGTGATTTGGGGTTTGGTATTGC 240
DB 6156 GTTGGCTTCGGAGCACATATTTGACATGTTGGACTGTGATTTGGGGTTTGGTATTGC 6215
QY 241 TCTGAATCCTAATGCTGTCTGCTTGGAGCATCTAGAATCTGAAATCTGTGTGTCAGAAATCT 300
DB 6216 TCTGAATCCTAATGCTGTCTGCTTGGAGCATCTAGAATCTGAAATCTGTGTGTCAGAAATCT 6275
QY 301 ATTATCTTGTAGTAGGACATCTCCAGTCTCTGCTTCTAGGGCTGAGAGTCTGTAGT 360
DB 6276 ATTATCTTGTAGTAGGACATCTCCAGTCTCTGCTTCTAGGGCTGAGAGTCTGTAGT 6335
QY 361 CAGTGACCCGCTCTGGCATTTTCAACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 420
DB 6336 CAGTGACCCGCTCTGGCATTTTCAACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 6395
QY 421 CAACCAACCAACCGAATAAACCATTTAGAACCTTTCCCACTTCCCTAGCTGCAATGTAA 480
DB 6396 CAACCAACCAACCGAATAAACCATTTAGAACCTTTCCCACTTCCCTAGCTGCAATGTAA 6455
QY 481 ACCTAGGATTTCTGTTTAAATAGGTTTCATATGAATTAATTCAGCTGATCAACCTTACAT 540
DB 6456 ACCTAGGATTTCTGTTTAAATAGGTTTCATATGAATTAATTCAGCTGATCAACCTTACAT 6515
QY 541 TCCTTTACCGTTATTTCTACACCCACCTTAAATGCAITTCCTGATATATTCCTGCTGAT 600
DB 6516 TCCTTTACCGTTATTTCTACACCCACCTTAAATGCAITTCCTGATATATTCCTGCTGAT 6575
QY 601 CTACCTATATAGTAAATCTCTGCTTTCAGAGTTTCTAGTGCATTAACATACCTGATTTA 660
DB 6576 CTACCTATATAGTAAATCTCTGCTTTCAGAGTTTCTAGTGCATTAACATACCTGATTTA 6635
QY 661 CATTCTTTTACTTTAAAGTGGAAATAAGAGTCCCTCTGACAGTTTCAGGAGTTCTCAAGA 720
DB 6636 CATTCTTTTACTTTAAAGTGGAAATAAGAGTCCCTCTGACAGTTTCAGGAGTTCTCAAGA 6695
QY 721 TGGCCCTTACTTTCTGACATCAATTTAGAGATTTCAAGGAGTGGCCAGAGATCATCTCAGT 780
DB 6696 TGGCCCTTACTTTCTGACATCAATTTAGAGATTTCAAGGAGTGGCCAGAGATCATCTCAGT 6755
QY 781 TCAGTGATTTGCTGTAGTCCCTCATATAAATCAATGAAGCTTTATGCTCATGGCTATGG 840
DB 6756 TCAGTGATTTGCTGTAGTCCCTCATATAAATCAATGAAGCTTTATGCTCATGGCTATGG 6815
QY 841 TTTATTACAGCAAAAGAAATAGAGTAAATCTAGCAAGGAGAGTTGATGGGGCAAA 900
DB 6816 TTTATTACAGCAAAAGAAATAGAGTAAATCTAGCAAGGAGAGTTGATGGGGCAAA 6875
QY 901 GACAGGAGCTCCAGTCCAGAGTTCCTGTTGTTTCTCCAGTGGGTGATGAAA 960
DB 6876 GACAGGAGCTCCAGTCCAGAGTTCCTGTTGTTTCTCCAGTGGGTGATGAAA 6935
QY 961 GCAGTATCTTCTCCATACAAATGATGTGTGATAATATTTCAGTGTATTGCCAATCAGGAAAC 1020
DB 6936 GCAGTATCTTCTCCATACAAATGATGTGTGATAATATTTCAGTGTATTGCCAATCAGGAAAC 6995
QY 1021 TCACTGAGCCTTGATTTATTTGAGCTTGGTTGACAGACATGTGACACCTTCATGG 1080
DB 6996 TCACTGAGCCTTGATTTATTTGAGCTTGGTTGACAGACATGTGACACCTTCATGG 7055
QY 1081 CTGAATCTTTAGTACTTAGCCCCCTCCAGACGTCTACAGCTGATAGGCTGTAAACCAACAT 1140
DB 7056 CTGAATCTTTAGTACTTAGCCCCCTCCAGACGTCTACAGCTGATAGGCTGTAAACCAACAT 7115
QY 1141 GTACCCATAAATCAATTTGTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 1200
DB 7116 GTACCCATAAATCAATTTGTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 7175
QY 1201 GCCTCTAAACAGGACAGGATATTTCAAAGCTTAGAGATGACCTCCAGAGCTGAATGC 1260

Db 7176 GCACCTTAAACAGCAGATATTTCAAAGCTTTAGAGATGACCTCCACGAGAGCTGAATGC 7235
Qy 1261 AAAGACCTGGCCCTTTTGGCGAAGAGATCCCTTTTACCGCACACTCTCTCTTTCACAGGGTT 1320
Db 7236 AAAGACCTGGCCCTTTTGGCGAAGAGATCCCTTTTACCGCACACTCTCTCTTTCACAGGGTT 7295
Qy 1321 ATTGTGAGGATCAAAATGTGTGTCATGTGTGAGACACACAGCACATGTGTGGCTGTGGAGA 1380
Db 7296 ATTGTGAGGATCAAAATGTGTGTCATGTGTGAGACACACAGCACATGTGTGGCTGTGGAGA 7355
Qy 1381 GTGACTTCTATGTGTCTAAACATTTGCTGAGTGTCTAAGAAAGTATTAGGATGGCTTTTCAG 1440
Db 7356 GTGACTTCTATGTGTCTAAACATTTGCTGAGTGTCTAAGAAAGTATTAGGATGGCTTTTCAG 7415
Qy 1441 CACTCAGATGTCTATCTAATCTCTCAACATGTGGCTACAGGTGGGCACTACTAGCCTC 1500
Db 7416 CACTCAGATGTCTATCTAATCTCTCAACATGTGGCTACAGGTGGGCACTACTAGCCTC 7475
Qy 1501 ATTTGACAGAGAAAGGACTGTGATAAGAAAGGGGTGACCAATAGTCAAGTCAATCTT 1560
Db 7476 ATTTGACAGAGAAAGGACTGTGATAAGAAAGGGGTGACCAATAGTCAAGTCAATCTT 7535
Qy 1561 GGATGCAAGGGGCTCCAGAGCAATGATTTAGACATTTGCTGACAGAAATTAATGCTGG 1620
Db 7536 GGATGCAAGGGGCTCCAGAGCAATGATTTAGACATTTGCTGACAGAAATTAATGCTGG 7595
Qy 1621 ATGTCTCTGCCCGAAGGGGATGCATTTCTTTGACCCCTATCTCAGATCTTGACT 1680
Db 7596 ATGTCTCTGCCCGAAGGGGATGCATTTCTTTGACCCCTATCTCAGATCTTGACT 7655
Qy 1681 TTGAGGTTATCTCAGACTTCTCTATGATACAGGAGCCCATCAATATCTCTCTGTGTC 1740
Db 7656 TTGAGGTTATCTCAGACTTCTCTATGATACAGGAGCCCATCAATATCTCTCTGTGTC 7715
Qy 1741 TCTCCCTCTCTCAGTCTTACTGCGCACTCTTCCAGTCCATCTCAGCTGCCAGGTG 1800
Db 7716 TCTCCCTCTCTCAGTCTTACTGCGCACTCTTCCAGTCCATCTCAGCTGCCAGGTG 7775
Qy 1801 TAGCCACAGTACCTAATCTTTGACAGAACTATAATGTGTATCTTACAGGGGAGAAA 1860
Db 7776 TAGCCACAGTACCTAATCTTTGACAGAACTATAATGTGTATCTTACAGGGGAGAAA 7835
Qy 1861 AAAAAAGAACTCTGAAAGAGCTGACATTTTACCGATTTGCAACACATTAAGTAACTCTG 1920
Db 7836 AAAAAAGAACTCTGAAAGAGCTGACATTTTACCGATTTGCAACACATTAAGTAACTCTG 7895
Qy 1921 CCAGTTTGTGCTGTGATGATCAGTCTGAGACTCTGGGTGAGGCAAGAAAGATTTTATAC 1980
Db 7896 CCAGTTTGTGCTGTGATGATCAGTCTGAGACTCTGGGTGAGGCAAGAAAGATTTTATAC 7955
Qy 1981 CCAGCTAAGGAGGAGCAGTGAATTTGTGTTTACATTTTGTTCACATTTTGTCCCCCAAT 2040
Db 7956 CCAGCTAAGGAGGAGCAGTGAATTTGTGTTTACATTTTGTTCACATTTTGTCCCCCAAT 8015
Qy 2041 CATATGGATGATCAGAGCAGTTTCTGAGTGGATGGACACAGGGTTTGTGCAAGGTGAG 2100
Db 8016 CATATGGATGATCAGAGCAGTTTCTGAGTGGATGGACACAGGGTTTGTGCAAGGTGAG 8075
Qy 2101 CAACCTAGGCTTAGAAATCTCTCAATCTTATAAGAAAGTACTAGCAAACTTTGTCCAGTCTT 2160
Db 8076 CAACCTAGGCTTAGAAATCTCTCAATCTTATAAGAAAGTACTAGCAAACTTTGTCCAGTCTT 8135
Qy 2161 TGTATCTGACGAGATATTAATCTTTTAAATTTGGTTGAAAGCAGACCTACTCTGAGGAA 2220
Db 8136 TGTATCTGACGAGATATTAATCTTTTAAATTTGGTTTGAAGCAGACCTACTCTGAGGAA 8195
Qy 2221 CATATTGTATTTATTTGCTGAAACAGTAAACAAATCTGCTGTAATATAGACGTTAACTTT 2280
Db 8196 CATATTGTATTTATTTGCTGAAACAGTAAACAAATCTGCTGTAATATAGACGTTAACTTT 8255
Qy 2281 ATTAATGAGCAGTAAGCAAACTTAGATCTGAAGGCGATACCATCTTGAAGGCTATCT 2340
Db 8256 ATTAATGAGCAGTAAGCAAACTTAGATCTGAAGGCGATACCATCTTGAAGGCTATCT 8315

Qy 2341 GCTGTCAAAATATGCTTGAAGAAGTGTCCAGAAAAAGAAAAACGGTATTATTATTCCTTTGCT 2400
Db 8316 GCTGTCAAAATATGCTTGAAGAAGTGTCCAGAAAAAGAAAAACGGTATTATTATTCCTTTGCT 8375
Qy 2401 CAGRAGACACAGAAACATTAAGAAACCATTAAGAAATTTGCTCCCAACACTGTTCAACC 2460
Db 8376 CAGRAGACACAGAAACATTAAGAAACCATTAAGAAATTTGCTCCCAACACTGTTCAACC 8435
Qy 2461 AGAGCCTTCCACTCTTGTCTGACGACAGTCTTAAACATCCCATCATTAATAGTGTGTACCA 2520
Db 8436 AGAGCCTTCCACTCTTGTCTGACGACAGTCTTAAACATCCCATCATTAATAGTGTGTACCA 8495
Qy 2521 CATCTGGCTTCAACCGTGCCTAAACAGATTTCTAGGTCCAGTTCCTCCACCATGTTGGCA 2580
Db 8496 CATCTGGCTTCAACCGTGCCTAAACAGATTTCTAGGTCCAGTTCCTCCACCATGTTGGCA 8555
Qy 2581 GTGCCCCACTGCCCCAACCCAGAAATTAAGGAGTGTCTCAGAAATTCGAGGGGACATGGGTGG 2640
Db 8556 GTGCCCCACTGCCCCAACCCAGAAATTAAGGAGTGTCTCAGAAATTCGAGGGGACATGGGTGG 8615
Qy 2641 GGATCAGAACTTCTGGGCTTGAAGTGCAGAGGGGGCCCATCTCTTGGTTCCGAAGGAGG 2700
Db 8616 GGATCAGAACTTCTGGGCTTGAAGTGCAGAGGGGGCCCATCTCTTGGTTCCGAAGGAGG 8675
Qy 2701 AAGAGGCTGGAGGTGAATGTCTTGGAGGGGAGAAATGTGGGTCTCTGAATCTTTAAATCC 2760
Db 8676 AAGAGGCTGGAGGTGAATGTCTTGGAGGGGAGAAATGTGGGTCTCTGAATCTTTAAATCC 8735
Qy 2761 CCAAGGAGGAGACTGTGAAGTCCAGCTTCCAGGTACTGACGTGGAAATGGCCTGAG 2820
Db 8736 CCAAGGAGGAGACTGTGAAGTCCAGCTTCCAGGTACTGACGTGGAAATGGCCTGAG 8795
Qy 2821 AGGCTTAGAATCCCGTATCTCGGGAAGAGGGGCTGAAATGTGAGGGGTGAGTTGC 2880
Db 8796 AGGCTTAGAATCCCGTATCTCGGGAAGAGGGGCTGAAATGTGAGGGGTGAGTTGC 8855
Qy 2881 AGGGGTGTTGTAGCTTGAGACTCTCTTGGTGGTCCCTGGGAAAGCAAGGACTGGAAACCAT 2940
Db 8856 AGGGGTGTTGTAGCTTGAGACTCTCTTGGTGGTCCCTGGGAAAGCAAGGACTGGAAACCAT 8915
Qy 2941 GGCTCAGGGTTTGGTGTGAAGTAAATGGGATCTCTGATCTTCAAGAGGTCAGAGGACT 3000
Db 8916 GGCTCAGGGTTTGGTGTGAAGTAAATGGGATCTCTGATCTTCAAGAGGTCAGAGGACT 8975
Qy 3001 GAGAGTTGCCATGCTTTGATCTTTTCCATCTACTCTTACTCTTACTCTGAGGGTAAATCACC 3060
Db 8976 GAGAGTTGCCATGCTTTGATCTTTTCCATCTACTCTTACTCTTACTCTGAGGGTAAATCACC 9035
Qy 3061 TACTCTTCTAGTTCCAAAGAGTGGCCTGGCGAGTATAATCTGCACATGTGCCATGTC 3120
Db 9036 TACTCTTCTAGTTCCAAAGAGTGGCCTGGCGAGTATAATCTGCACATGTGCCATGTC 9095
Qy 3121 CCGAGGCTGGGCACTATCCACTCATCTCAGCATCTGGCATATCGGGCGAGGCGCG 3180
Db 9096 CCGAGGCTGGGCACTATCCACTCATCTCAGCATCTGGCATATCGGGCGAGGCGCG 9155
Qy 3181 CGCCATGACGTCAATAGCTGCACTATCCCTGAGCGGCTCTCCCGTCACTGTCACGTTCCAA 3240
Db 9156 CGCCATGACGTCAATAGCTGCACTATCCCTGAGCGGCTCTCCCGTCACTGTCACGTTCCAA 9215
Qy 3241 CCATGGAGCTGTGGAGCTGGCTCCCTGGTGGATCTGGCTGGCTGGCTGGCTGGCTGGCTGG 3300
Db 9216 CCATGGAGCTGTGGAGCTGGCTCCCTGGTGGATCTGGCTGGCTGGCTGGCTGGCTGGCTGG 9275
Qy 3301 CCTGTGTCCGATAAAGATCTCTAGAACCCACAGGAAACCCAGGACTGAAAGGTGCTAGAGAA 3360
Db 9276 CCTGTGTCCGATAAAGATCTCTAGAACCCACAGGAAACCCAGGACTGAAAGGTGCTAGAGAA 9335
Qy 3361 TGGCCATATGTCGCTGTCCATGAAATCTCAGGACTTCTGGGTGGAGGGCACAGAGGCT 3420
Db 9336 TGGCCATATGTCGCTGTCCATGAAATCTCAGGACTTCTGGGTGGAGGGCACAGAGGCT 9395

1081 QY CTGAACCTTTAGTACTTAGCCCTCCAGACGCTACAGCTGATAGGCTGTAAACCAACATT 1140
7056 Db CTGAACCTTTAGTACTTAGCCCTCCAGACGCTACAGCTGATAGGCTGTAAACCAACATT 7115
1141 QY GTCAACATAAATCACATTTGTAGACTATCCAGTGTGCGCCCAAGCTCCCGGTGTAAACACAG 1200
7116 Db GTCAACATAAATCACATTTGTAGACTATCCAGTGTGCGCCCAAGCTCCCGGTGTAAACACAG 7175
1201 QY GCACCTTAAACAGCGAGATATTTCAAAGCTTTAGAGATGACCTCCAGAGCTGAATGC 1260
7176 Db GCACCTTAAACAGCGAGATATTTCAAAGCTTTAGAGATGACCTCCAGAGCTGAATGC 7235
1261 QY AAGACCTGCGCTCTTTGGCAGAGGAAATCCCTTTACCGCACACTCTCCCTCACAGGTT 1320
7236 Db AAGACCTGCGCTCTTTGGCAGAGGAAATCCCTTTACCGCACACTCTCCCTCACAGGTT 7295
1321 QY ATTGTGAGGATCAAAATGTGCTCATGTGTGTGACACACAGCACATGTCTGGCTGTGGAGA 1380
7296 Db ATTGTGAGGATCAAAATGTGCTCATGTGTGTGACACACAGCACATGTCTGGCTGTGGAGA 7355
1381 QY GTGACTTCTATGTGTCTACATTTGCTGAGTGTCTAGAGTATTAAGGATGGCTTTGAG 1440
7356 Db GTGACTTCTATGTGTCTACATTTGCTGAGTGTCTAGAGTATTAAGGATGGCTTTGAG 7415
1441 QY CACTCACAGATGCTCATCTAATCCTCAACATGCTTACAGGCTGGGCACACTAGCCCTC 1500
7416 Db CACTCACAGATGCTCATCTAATCCTCAACATGCTTACAGGCTGGGCACACTAGCCCTC 7475
1501 QY ATTGTACAGAGGAAGGACTGTGGATGAAGAGGGGTGACCAATAGGTACAGTCAATCT 1560
7476 Db ATTGTACAGAGGAAGGACTGTGGATGAAGAGGGGTGACCAATAGGTACAGTCAATCT 7535
1561 QY GGATGCAAGGGGCTCCAGAGGACCATGATTAGACATTTGCTGCAGAGAAATTAAGCTGG 1620
7536 Db GGATGCAAGGGGCTCCAGAGGACCATGATTAGACATTTGCTGCAGAGAAATTAAGCTGG 7595
1621 QY ATGTCTCTGCCCGGAAAGGGGATGCATTTCTTTGAACCCCTATCTCAGATCTTTGACT 1680
7596 Db ATGTCTCTGCCCGGAAAGGGGATGCATTTCTTTGAACCCCTATCTCAGATCTTTGACT 7655
1681 QY TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCCCATATATCTCTGTGTGTC 1740
7656 Db TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCCCATATATCTCTGTGTGTC 7715
1741 QY TCTCCCTCTCCTCAGTCTTACTGCCACTCTTCCAGCTCCATCTCAGGTGCCAGGTG 1800
7716 Db TCTCCCTCTCCTCAGTCTTACTGCCACTCTTCCAGCTCCATCTCAGGTGCCAGGTG 7775
1801 QY TAGCCACAGTACCTAATCTTTGAGAGAACTATAATGTGTATCTACAGGGGAGAAA 1860
7776 Db TAGCCACAGTACCTAATCTTTGAGAGAACTATAATGTGTATCTACAGGGGAGAAA 7835
1861 QY AAAAAAAGAACTCTGAAGAGCTGACATTTTACCGACTTCGAAACACATAAGCTAACCTG 1920
7836 Db AAAAAAAGAACTCTGAAGAGCTGACATTTTACCGACTTCGAAACACATAAGCTAACCTG 7895
1921 QY CCAGTTTGTGCTGGTGAAGTCTATGAGACTCTCTGGGTGAGAGCAAGATTTTATAC 1980
7896 Db CCAGTTTGTGCTGGTGAAGTCTATGAGACTCTCTGGGTGAGAGCAAGATTTTATAC 7955
1981 QY CCAGCTTAAGGAGGAGCATGAATTTGTGTTTACATTTGTTTACCTTTGCCCCCAATT 2040
7956 Db CCAGCTTAAGGAGGAGCATGAATTTGTGTTTACATTTGTTTACCTTTGCCCCCAATT 8015
2041 QY CATATGGATGATCAGAGCAGTTCAGGTGATGAGACACAGGGTTTGTGCAAGGTGAG 2100
8016 Db CATATGGATGATCAGAGCAGTTCAGGTGATGAGACACAGGGTTTGTGCAAGGTGAG 8075
2101 QY CAACCTAGGCTTAGAATCTCAATCTTATGAAGGTTACTAGCAACTTTGTCAGTCTT 2160
8076 Db CAACCTAGGCTTAGAATCTCAATCTTATGAAGGTTACTAGCAACTTTGTCAGTCTT 8135
2161 QY TGATATGACGGAGATATTATCTTTTAAATTTGGGTTGAAAAGCAGACCTACTCTGAGGAA 2220

8136 Db TGATATGACGGAGATATTATCTTTAAATTTGGGTTGAAAAGCAGACCTACTCTCGAGGAA 8195
2221 QY CATATTGTATTATTATGCTCTGAAACAGTAAACAAATCTGCTGTAAATAGACGTTTAACTTT 2280
8196 Db CATATTGTATTATTATGCTCTGAAACAGTAAACAAATCTGCTGTAAATAGACGTTTAACTTT 8255
2281 QY ATTATCTAAGCGAGTAAGCAAAACCTAGATCTGAAGGCGATACCATTCTTGAAGGCTATCT 2340
8256 Db ATTATCTAAGCGAGTAAGCAAAACCTAGATCTGAAGGCGATACCATTCTTGAAGGCTATCT 8315
2341 QY GCTGTACAAATATGCTTGAAGAGATGGTCCAGAAAAAGAAAAACGGTATTATTTCCTTTGCT 2400
8316 Db GCTGTACAAATATGCTTGAAGAGATGGTCCAGAAAAAGAAAAACGGTATTATTTCCTTTGCT 8375
2401 QY CAGAAAGACACACAGAAACATAAGAGAACCTAGGTAAGTCTCCGAAACACTGTTCAACC 2460
8376 Db CAGAAAGACACACAGAAACATAAGAGAACCTAGGTAAGTCTCCGAAACACTGTTCAACC 8435
2461 QY AGAGCCTTCCACTCTTGTCTCAGACAGTCTTAACATCCCATCATATTAGTGTCTACCA 2520
8436 Db AGAGCCTTCCACTCTTGTCTCAGACAGTCTTAACATCCCATCATATTAGTGTCTACCA 8495
2521 QY CATCTGGCTTCAACCGTGCCTAAACCAAGATTTCTAGGTTCCAGTTCCTCCCAACCATGTTGGCA 2580
8496 Db CATCTGGCTTCAACCGTGCCTAAACCAAGATTTCTAGGTTCCAGTTCCTCCCAACCATGTTGGCA 8555
2581 QY GTGCCCCACTGCAACCCAGAAATAAGGGAGTGTCTCAGAAATTCGAGGGGACATGGGTGG 2640
8556 Db GTGCCCCACTGCAACCCAGAAATAAGGGAGTGTCTCAGAAATTCGAGGGGACATGGGTGG 8615
2641 QY GGATCAGAACTTCTGGGCTTGAAGTGCAGAGAGGGGCCCACTACTCTCTTGGTTCGGAAGGAGG 2700
8616 Db GGATCAGAACTTCTGGGCTTGAAGTGCAGAGAGGGGCCCACTACTCTCTTGGTTCGGAAGGAGG 8675
2701 QY AAGAGCTGAGGTGAATGTCTTGGAGGGGAGGAAATGTGGGTTCTGAACCTTTAAATCC 2760
8676 Db AAGAGCTGAGGTGAATGTCTTGGAGGGGAGGAAATGTGGGTTCTGAACCTTTAAATCC 8735
2761 QY CCAAGGAGGAGACTGTGAAGTCCAGCTTCCAGGTACTCTGAGTGGGAAATGSCCTGAG 2820
8736 Db CCAAGGAGGAGACTGTGAAGTCCAGCTTCCAGGTACTCTGAGTGGGAAATGSCCTGAG 8795
2821 QY AGGTCTAAGAAATCCGTAATCTCGGGAAGGAGGGGCTGAAATTTGTAGGGGTTGAGTTGC 2880
8796 Db AGGTCTAAGAAATCCGTAATCTCGGGAAGGAGGGGCTGAAATTTGTAGGGGTTGAGTTGC 8855
2881 QY AGGGGTTTGTAGCTTGAGACTCTTGTGTGGTCCCTGGGAAGCAAGACTGGGAACCAATT 2940
8856 Db AGGGGTTTGTAGCTTGAGACTCTTGTGTGGTCCCTGGGAAGCAAGACTGGGAACCAATT 8915
2941 QY GGCTCCAGGGTTGGTGTGAAGGTAATGGGATCTCTGATTTCTCAAAGGGTCAGAGGACT 3000
8916 Db GGCTCCAGGGTTGGTGTGAAGGTAATGGGATCTCTGATTTCTCAAAGGGTCAGAGGACT 8975
3001 QY GAGAGTTCCTCATGCTTTGATCTTCCATCTACTCTTCTACTCTTCCACTTGGAGGTAATCACC 3060
8976 Db GAGAGTTCCTCATGCTTTGATCTTCCATCTACTCTTCTACTCTTCCACTTGGAGGTAATCACC 9035
3061 QY TACTCTTCTAGTTCACAAAGAGTGGCCTGCGAGTATAATCTGCACATGTGCCATGTC 3120
9036 Db TACTCTTCTAGTTCACAAAGAGTGGCCTGCGAGTATAATCTGCACATGTGCCATGTC 9095
3121 QY CCGAGGCTTGGGCTCATCCACTCATCTTCCAGCATCTGGCTATGGGGGAGGCGG 3180
9096 Db CCGAGGCTTGGGCTCATCCACTCATCTTCCAGCATCTGGCTATGGGGGAGGCGG 9155
3181 QY CGCCATGACGTCATGTAGCTGCGACTATCCCTGAGCGCGCTCTCCCGTCACTGCCCAA 3240
9156 Db CGCCATGACGTCATGTAGCTGCGACTATCCCTGAGCGCGCTCTCCCGTCACTGCCCAA 9215
3241 QY CCATGAGCTGTGAGCGTGGTCCCTGCTGGTGAATGTGGCTCTGGTGTGCAGGCGCGGG 3300

Db 9216 CCATGGAGCTGTGACGTGCGTCCCTCGTGGATGTGCGCTGCGTGGTCCAGGCCGGG 9275
Qy 3301 CCTGGTGTCCGATAAAGATCTTAGAACACACAGGAACAGGACTGAAAGTGTAGAGAA 3360
Db 9276 CCTGGTGTCCGATAAAGATCTTAGAACACACAGGAACAGGACTGAAAGTGTAGAGAA 9335
Qy 3361 TGGCCATATGTCGTGTCCTCATGAATCTCAAGGACTTCTGGGTGGAGGACACAGGAGCCT 3420
Db 9336 TGGCCATATGTCGTGTCCTCATGAATCTCAAGGACTTCTGGGTGGAGGACACAGGAGCCT 9395
Qy 3421 GAATTCACGGTGTGCCCCAGTCCACTGCTCCCAAGTGAAGTCTCCAGATACAGAGCA 3480
Db 9396 GAATTCACGGTGTGCCCCAGTCCACTGCTCCCAAGTGAAGTCTCCAGATACAGAGCA 9455
Qy 3481 CTGTGCGCAGCATGAGTTCATCTGTACCATCTTCTTACAGGACTACCCAGGACCCCTG 3540
Db 9456 CTGTGCGCAGCATGAGTTCATCTGTACCATCTTCTTACAGGACTACCCAGGACCCCTG 9515
Qy 3541 ATGAACACCATGTGTGTGAGGAAGAGGGGTGAAGGATGACCTCTGTGTGTGTCAGA 3600
Db 9516 ATGAACACCATGTGTGTGAGGAAGAGGGGTGAAGGATGACCTCTGTGTGTGTCAGA 9575
Qy 3601 GCCAGAGGGGCGCATACCGGTGGGAGGAGGAGCTGTGACTGGC 3645
Db 9576 GCCAGAGGGGCGCATACCGGTGGGAGGAGGAGCTGTGACTGGC 9620

RESULT 8
ACD07307
ID ACD07307 standard; DNA; 12047 BP.
XX AC ACD07307;
XX DT 07-AUG-2003 (first entry)
XX DE Human glandular kallikrein (hKlK) TRE.
XX KW Adenoviral vector; adenovirus gene; transcriptional control; TRE;
XX cell type-specific; transcriptional response element; PSA; hKlK;
XX prostate-specific antigen; glandular kallikrein; probastin; PB;
XX carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUC1;
XX cytotoxicity; neoplasia; tumour growth; gene therapy; cytostatic; human;
XX ds.
XX OS Homo sapiens.
XX PN US2003044383-A1.
XX PD 06-MAR-2003.
XX PF 10-SEP-1998; 98US-00151376.
XX PR 27-JUN-1995; 95US-00495034.
XX PR 20-AUG-1996; 96US-00699753.
XX PR 03-MAR-1997; 97US-0039597P.
XX PR 03-MAR-1997; 97US-0039599P.
XX PR 03-MAR-1997; 97US-0039762P.
XX PR 03-MAR-1997; 97US-0039763P.
XX PR 02-MAR-1998; 98US-00033333.
XX PR 02-MAR-1998; 98US-00033428.
XX PR 02-MAR-1998; 98US-00033555.
XX PA (HEND/) HENDERSON D R.
XX PA (SCHU/) SCHUUR E R.
XX FI Henderson DR, Schuur ER;
XX WP1; 2003-456547/43.
XX PT New adenovirus vector for transfecting target host cells, comprises an
XX adenovirus gene under transcriptional control of a cell type-specific
XX transcriptional response element.

PS Disclosure; Fig 16; 83pp; English.
XX The present invention relates to adenoviral vectors comprising an
adenovirus gene under transcriptional control of a cell type-specific
transcriptional response element (TRE). Example TREs given in the
specification include human prostate-specific antigen (PSA) TRE, human
glandular kallikrein (hKlK) TRE, rat probastin (PB) TRE, human
carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3
(MUC1) TRE. The modified adenovirus vector is useful as a vehicle for
introducing new genetic capability, particularly associated with
cytotoxicity for treating neoplasia. For example, the vector may be used
in a target cell to suppress tumour growth, or to kill the target cell.
The vector is particularly useful in gene therapy. The present sequence
represents a TRE

XX Sequence 12047 BP; 3051 A; 2484 C; 2869 G; 3643 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 3645; DB 7; Length 12047;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCCTCAATAATTTGTTAAGAGTCTAAATGTGTCCAAAGATGGAATGTTTGAGAATA 60
Db 5976 GGCCCTCAATAATTTGTTAAGAGTCTAAATGTGTCCAAAGATGGAATGTTTGAGAATA 6035
Qy 61 CTGTCCAGAGATTTTCTGAGTCTTAGAGTGTGGAAATATAGAACTGAGCTTGGCTT 120
Db 6036 CTGTCCAGAGATTTTCTGAGTCTTAGAGTGTGGAAATATAGAACTGAGCTTGGCTT 6095
Qy 121 CTTGAGCTAGAACTCAGGAGTATGGGCTGAAGTCTGAAGCTTGGCTTCAGCAGTTGGG 180
Db 6096 CTTGAGCTAGAACTCAGGAGTATGGGCTGAAGTCTGAAGCTTGGCTTCAGCAGTTGGG 6155
Qy 181 GTTGGCTTCGGAGCACATATTTGACATGTTGGACATGTGATTTGGGTTTGGTATTTCG 240
Db 6156 GTTGGCTTCGGAGCACATATTTGACATGTTGGACATGTGATTTGGGTTTGGTATTTCG 6215
Qy 241 TCTGAATCTTAATGTCGTCTTGAGGCATCTAGAACTGAAATCTGTGTGCAATTTCT 300
Db 6216 TCTGAATCTTAATGTCGTCTTGAGGCATCTAGAACTGAAATCTGTGTGCAATTTCT 6275
Qy 301 ATTAATCTGAGTAGACATCTCCAGTCTCTGGTCTCTGCTTCTAGGGCTGAGTCTGTAGT 360
Db 6276 ATTAATCTGAGTAGACATCTCCAGTCTCTGGTCTCTGCTTCTAGGGCTGAGTCTGTAGT 6335
Qy 361 CAGTGACCCGGTCTGGCATTTCAACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 420
Db 6336 CAGTGACCCGGTCTGGCATTTCAACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 6395
Qy 421 CAACCAACACCGAATAAACCATTGCAACCTTCCCACTTCCCTAGCTGCAATGTTAA 480
Db 6396 CAACCAACACCGAATAAACCATTGCAACCTTCCCACTTCCCTAGCTGCAATGTTAA 6455
Qy 481 ACCTAGGATTTCTGTTTAATAGTTCATATGAATAATTTTCAGCTGATCAACCTTACAT 540
Db 6456 ACCTAGGATTTCTGTTTAATAGTTCATATGAATAATTTTCAGCTGATCAACCTTACAT 6515
Qy 541 TCCCTTACCGTTCATCTACACCCACCTTAAATGCAATCCCAATATATTTCCCTGATTT 600
Db 6516 TCCCTTACCGTTCATCTACACCCACCTTAAATGCAATCCCAATATATTTCCCTGATTT 6575
Qy 601 CTACCTATATATGTAATCTCTGGCTTTGCCAGTTTCTTAGTGCATTAACATACCTGATTTA 660
Db 6576 CTACCTATATATGTAATCTCTGGCTTTGCCAGTTTCTTAGTGCATTAACATACCTGATTTA 6635
Qy 661 CATCTTTTACTTTAAAGTGGAAATAGAGTCCCTCTGAGAGTTTCAGGAGTTCTCAAGA 720
Db 6636 CATCTTTTACTTTAAAGTGGAAATAGAGTCCCTCTGAGAGTTTCAGGAGTTCTCAAGA 6695
Qy 721 TGGCCCTTACTTCTGACATCAATTTGAGATTTCAAGGGAGTCCGCAAGATCATCTCAGGT 780
Db 6696 TGGCCCTTACTTCTGACATCAATTTGAGATTTCAAGGGAGTCCGCAAGATCATCTCAGGT 6755

QY 781 TCAGTGATGCTGGTAGCCCTCATATAACTCAATGAAAGCTGTATGCTCATGGCTATGG 840
Db |||||
QY 6756 TCAGTGATGCTGGTAGCCCTCATATAACTCAATGAAAGCTGTATGCTCATGGCTATGG 6815
Db |||||
QY 841 TTTATTACAGCAAAAGAAATAGAGATGAAATCTAGCAAGGGAAGAGTTGCATGGGCAAA 900
Db |||||
QY 6816 TTTATTACAGCAAAAGAAATAGAGATGAAATCTAGCAAGGGAAGAGTTGCATGGGCAAA 6875
Db |||||
QY 901 GACNAGAGAGCTCCAGTGCAGAGATTCCTGTGTTTCTCCAGTGGTGTGTCATGAAA 960
Db |||||
QY 6876 GACNAGAGAGCTCCAGTGCAGAGATTCCTGTGTTTCTCCAGTGGTGTGTCATGAAA 6935
Db |||||
QY 961 GCAGTATCTTCTCCATAACAATGATGTGTGATAATATTCAGTGTATTCGCAACACCTTCATGG 1020
Db |||||
QY 6936 GCAGTATCTTCTCCATAACAATGATGTGTGATAATATTCAGTGTATTCGCAACACCTTCATGG 6995
Db |||||
QY 1021 TCAACTCAGGCTTGATTTATATTTGAGGCTTGCTGTCACAGACATGTGCAACACCTTCATGG 1080
Db |||||
QY 6996 TCAACTCAGGCTTGATTTATATTTGAGGCTTGCTGTCACAGACATGTGCAACACCTTCATGG 7055
Db |||||
QY 1081 CTGAACCTTTAGTACTTAGCCCTCCAGACGTCTACAGCTGATAGGCTGTAAACCAACATT 1140
Db |||||
QY 7056 CTGAACCTTTAGTACTTAGCCCTCCAGACGTCTACAGCTGATAGGCTGTAAACCAACATT 7115
Db |||||
QY 1141 GTCACCAATAATCAATTTGTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 1200
Db |||||
QY 7116 GTCACCAATAATCAATTTGTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 7175
Db |||||
QY 1201 GCACCTTAACAGCAGGATATTTCAAAGCTTAGAGATGACCTCCAGGAGCTGAATGC 1260
Db |||||
QY 7176 GCACCTTAACAGCAGGATATTTCAAAGCTTAGAGATGACCTCCAGGAGCTGAATGC 7235
Db |||||
QY 1261 AAAGACCTGGCTCTTTGGCAAGGGAATCCTTTACCGCACACTCTCTTTCACAGGGTT 1320
Db |||||
QY 7236 AAAGACCTGGCTCTTTGGCAAGGGAATCCTTTACCGCACACTCTCTTTCACAGGGTT 7295
Db |||||
QY 1321 ATTGTGAGGATCAAAATGGTGTATGTGTGAGACAGCAGACATGTGTGGCTGTGGAGA 1380
Db |||||
QY 7296 ATTGTGAGGATCAAAATGGTGTATGTGTGAGACAGCAGACATGTGTGGCTGTGGAGA 7355
Db |||||
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XX DT
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XX
XX (CALY-) CALYDON INC.
XX
XX Yu D, Herdenson DR, Schuur ER;
XX WPI; 1999-153804/13.
XX
XX New nucleic acid containing the human glandular kallikrein enhancer -
XX providing increased expression of heterologous sequences in prostatic
XX cells, and related adenoviral vectors for treating prostatic cancer.
XX
XX Claim 1; Page 150-157; 179pp; English.
XX
XX This polynucleotide comprises the promoter/enhancer region of the human
XX glandular kallikrein (hK1 or hK2) gene. An hK2 enhancer, when
XX operably linked to an hK2 promoter and a reporter gene, increases
XX transcription of cis-linked sequences in prostatic cells in the presence
XX of androgen at levels 30-100 fold over the level of transcription in the
XX absence of androgen. The hK2 enhancer can form part of an hK2
XX transcriptional regulatory element (hK2-TRE), which in turn can be
XX operably linked to a heterologous polynucleotide to effect
XX transcriptional control of a linked gene. The hK2-TRE is useful for
XX enabling the directed expression of a desired gene in these cells. The
XX hK2-TRE can be incorporated into a replication-competent adenovirus
XX vector so that the hK2-TRE controls expression of at least one
XX adenoviral gene, preferably one that contributes to cytotoxicity. Such
XX vectors are useful for treatment of cancers such as prostate cancer.
XX Methods for conferring selective cytotoxicity on a cell and for screening
XX compounds for the treatment of prostate cancer are claimed
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XX Sequence 12047 BP; 3053 A; 2482 C; 2870 G; 3642 T; 0 U; 0 Other;
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Qy 3546 CACCATGCTGTGTCAGGAGAGGGGTGAAGCATGCACTCTGTGTGTGTGTGTGTGTGTGTGT 3605
Db 9521 CACCATGCTGTGTCAGGAGAGGGGTGAAGCATGCACTCTGTGTGTGTGTGTGTGTGTGT 9580
Qy 3606 GAGGGGGCCATGACGGGTGGGGAGGAGGCTGTGGAATGGC 3645
Db 9581 GAGGGGGCCATGACGGGTGGGGAGGAGGCTGTGGAATGGC 9620

ID AAX24772 standard; DNA; 1172 BP.
XX AAX24772;
DT 21-JUN-1999 (first entry)
XX Human glandular kallikrein hK2 gene enhancer.
XX Enhancer; glandular kallikrein-1; hK1-1; hK2; human; prostate cancer;
KW therapy; androgen response element; ARE; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT misc_signal 993..1007
FT /*tag= a
FT /function= "androgen response element"
XX WO9906576-A1.
PN 11-FEB-1999.
PD 04-AUG-1998; 98WO-US016312.
PF 04-AUG-1997; 97US-0054523P.
PR 02-MAR-1998; 98US-0076545P.
PR 03-AUG-1998; 98US-00127834.
XX (CALY-) CALYDON INC.
XX Yu D, Herdenson DR, Schuur ER;
XX WPI; 1999-153804/13.
XX New nucleic acid containing the human glandular kallikrein enhancer -
PT providing increased expression of heterologous sequences in prostatic
PT cells, and related adenoviral vectors for treating prostatic cancer.
XX Claim 4; Page 168; 179pp; English.
XX This polynucleotide comprises nucleotides 7200-8371 of the 5' flanking
CC region of the human glandular kallikrein (hK2) gene (see AAX24755).
CC This comprises a claimed enhancer region including a putative androgen
CC response element (ARE). Mutation of this ARE (see AAX24773 and AAX24774)
CC was shown to affect enhancer function. hK2 enhancers of the invention
CC have been shown to increase the transcription of cis-linked coding
CC sequences in prostate cells. Methods of using DNA constructs comprising
CC the enhancers to control transcription of heterologous polynucleotides
CC are provided. Adenoviral vectors in which one or more genes are under
CC transcriptional control of a hK2 transcription regulatory element are
CC claimed, and can be used to confer selective cytotoxicity in mammalian
CC cells for use e.g. in the treatment of prostate cancer
XX Sequence 1172 BP; 334 A; 257 C; 268 G; 313 T; 0 U; 0 Other;
SQ
Query Match 32.2%; Score 1172; DB 2; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1225 CAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCTCTTTGGGCAAG 1284
Db 1 CAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCTCTTTGGGCAAG 60
Qy 1285 GAGAACTCTTACCGACACTCTCTTTCACAGGTTATTTGAGGATCAAAATGTGTCT 1344
Db 61 GAGAACTCTTACCGACACTCTCTTTCACAGGTTATTTGAGGATCAAAATGTGTCT 120
Qy 1345 GTGTGTGAGACACAGGACATGTCTGCTGTGAGAGTGTCTTCTATGTGTCTACATT 1404
Db 121 GTGTGTGAGACACAGGACATGTCTGCTGTGAGAGTGTCTTCTATGTGTCTACATT 180
Qy 1405 GCTGAGTGTGAAGAGTATTAGGCAATGCTTTCAGCACTTCAGATGCTCAATTC 1464

Db 181 GCTGAGTGCTAAGAAAGTATTAGGATGGCTTTTTCAGCACTCACAGATGCTCATCTAATCC 240
QY 1485 TCACAACATGGCTCAGGGTGGGCACTACTAGCCTCATTTGACAGAGAAAGGACTGTGG 1524
Db 241 TCACAACATGGCTCAGGGTGGGCACTACTAGCCTCATTTGACAGAGAAAGGACTGTGG 300
QY 1525 ATAAGAAGGGGTGACCAATAGGTACAGATCATTTCTGATGCAAGGGGCTCCAGAGGACC 1584
Db 301 ATAAGAAGGGGTGACCAATAGGTACAGATCATTTCTGATGCAAGGGGCTCCAGAGGACC 360
QY 1585 ATGATTAGACATGCTGTCAGAGAAATTAATGGCTGGATGTCTCTGCCCGGAAAGGGGGA 1644
Db 361 ATGATTAGACATGCTGTCAGAGAAATTAATGGCTGGATGTCTCTGCCCGGAAAGGGGGA 420
QY 1645 TGCACCTTCTTCCAGCCCTATCTCAGATCTTGACTTTGAGGTTATCTCAGACTTCTCT 1704
Db 421 TGCACCTTCTTCCAGCCCTATCTCAGATCTTGACTTTGAGGTTATCTCAGACTTCTCT 480
QY 1705 ATGATACAGGAGGCCATCATATAATCTCTGTGTCTCTCTGCCCTTCTCAGTCTTACTGC 1764
Db 481 ATGATACAGGAGGCCATCATATAATCTCTGTGTCTCTCTGCCCTTCTCAGTCTTACTGC 540
QY 1765 CCACCTTCCAGCTCCATCTCCAGCTGGCCAGGTGAGCCACAGTACCTAACTTTTGC 1824
Db 541 CCACCTTCCAGCTCCATCTCCAGCTGGCCAGGTGAGCCACAGTACCTAACTTTTGC 600
QY 1825 AGAAGACTATAATGTGTATCTCTACAGGGGAGAAAAAGAACTCTGAAAGAGCTG 1884
Db 601 AGAAGACTATAATGTGTATCTCTACAGGGGAGAAAAAGAACTCTGAAAGAGCTG 660
QY 1885 ACATTTACCGACTTGCAACACATATAGCTAACCTGCCAGTTTGTCTGGTAGAATCA 1944
Db 661 ACATTTACCGACTTGCAACACATATAGCTAACCTGCCAGTTTGTCTGGTAGAATCA 720
QY 1945 TGAGACTCTCTGGGTGAGAGGCAAAAGATTTTATACCCACAGCTTAAGGAGGAGCATGAA 2004
Db 721 TGAGACTCTCTGGGTGAGAGGCAAAAGATTTTATACCCACAGCTTAAGGAGGAGCATGAA 780
QY 2005 CTTTGTGTACATTTGTCTACTTTGCCCCCAATTCATATGGGATGATCAGAGCAGTTC 2064
Db 781 CTTTGTGTACATTTGTCTACTTTGCCCCCAATTCATATGGGATGATCAGAGCAGTTC 840
QY 2065 AGGTGGATGACACAGGGTGTGGCAAGGTGAGCAACTAGGCTTGAATCTCTCAA 2124
Db 841 AGGTGGATGACACAGGGTGTGGCAAGGTGAGCAACTAGGCTTGAATCTCTCAA 900
QY 2125 TCTTATAAGAGGTAAGCAAACTTCTCCAGTCTTTGTATCTGACGAGATATTATCTT 2184
Db 901 TCTTATAAGAGGTAAGCAAACTTCTCCAGTCTTTGTATCTGACGAGATATTATCTT 960
QY 2185 TATAATTTGGGTGAAAGCAGACCTACTCTGGAGGACATATTGTATTATTGTCCTGAAC 2244
Db 961 TATAATTTGGGTGAAAGCAGACCTACTCTGGAGGACATATTGTATTATTGTCCTGAAC 1020
QY 2245 AGTAAACAAATCTCTCTGTAATAAGAGCTTAACCTTTATTATCTAAGCGCATGAGCAACC 2304
Db 1021 AGTAAACAAATCTCTCTGTAATAAGAGCTTAACCTTTATTATCTAAGCGCATGAGCAACC 1080
QY 2305 TAGATCTGAAGGCGATACCAATCTTGAAGGCTATCTGCTGTACAAATATGCTTGAAAGA 2364
Db 1081 TAGATCTGAAGGCGATACCAATCTTGAAGGCTATCTGCTGTACAAATATGCTTGAAAGA 1140
QY 2365 TGGTCCAGAAAAGAAAACGGTATTATTGTCCTT 2396
Db 1141 TGGTCCAGAAAAGAAAACGGTATTATTGTCCTT 1172

RESULT 11

AAZ06494

ID AAZ06494 standard; DNA; 1172 BP.

XX

AC AAZ06494;

XX

DT 23-NOV-1999 (first entry)
XX hKLK2 enhancer of construct CN390.
DE
XX
KW prostate; cancer; drug assay; drug development; enhancer; promoter;
tumour; kallikrein; androgen regulation; prostate specific antigen;
construct; ss.
KW
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9941413-A2.
XX
PD 19-AUG-1999.
XX
PF 11-FEB-1999; 99WO-US0031117.
XX
PR 12-FEB-1998; 98US-00022732.
XX
XX (CALY-) CALYDON INC.
XX Henderson DR, Lamparski HG, Schuur ER, Yu DC;
XX MPI; 1999-527378/44.
DR
XX
PT Screening for compounds which inhibit prostate cancer using a cell line
containing a marker whose expression is responsive to therapeutically
active compounds.
PT
XX
FS Claim 6; Page 49; 50pp; English.
XX
CC This is the nucleotide sequence of the hKLK2 enhancer region contained in
construct CN390. hKLK2 is a member of the kallikrein family, as is the
prostate specific antigen (PSA), a chymotrypsin like protein that is
synthesized exclusively by normal hyperplastic, and malignant prostatic
epithelia. This tissue specific nature of PSA makes it an excellent
biomarker for identifying benign prostatic hyperplasia (BPH) and
prostatic carcinoma (CaP). Elevated levels of PSA are indicative of BPH
or CaP. Like PSA, hKLK2 is expressed exclusively in the prostate and is
up regulated by androgens, primarily by transcription activation. The
proteins also exhibit a high degree of amino acid sequence identity and
contain similar regulatory elements. The characterisation of genes whose
expression is limited to the prostate allows the development of screening
methods which can identify substances capable of specifically altering
the expression of prostate-specific genes
XX
SQ Sequence 1172 BP; 334 A; 257 C; 268 G; 313 T; 0 U; 0 Other;
Query Match 32.2%; Score 1172; DB 2; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1225 CAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCTCTTTGGGCAAG 1284
Db 1 CAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCTCTTTGGGCAAG 60
QY 1285 GAGAACTCTTACCCGACACTCTCCTTCACAGGCTTATTGTGAGGATCAATGTGTCAT 1344
Db 61 GAGAACTCTTACCCGACACTCTCCTTCACAGGCTTATTGTGAGGATCAATGTGTCAT 120
QY 1345 GTGTGTGAGACACCCAGCACATGCTGGGCTGTGGAGAGTGACTTCTATGTGTAAACATT 1404
Db 121 GTGTGTGAGACACCCAGCACATGCTGGGCTGTGGAGAGTGACTTCTATGTGTAAACATT 180
QY 1405 GCTGAGTGTGAAGAAAGTATTAGGATGGCTTTTACGACTCAGAGATGCTCATCTAATCC 1464
Db 181 GCTGAGTGTGAAGAAAGTATTAGGATGGCTTTTACGACTCAGAGATGCTCATCTAATCC 240
QY 1465 TCACAACATGGCTCAGGGTGGGCACTACTAGCCTCATTTGACAGAGAAAGGACTGTGG 1524
Db 241 TCACAACATGGCTCAGGGTGGGCACTACTAGCCTCATTTGACAGAGAAAGGACTGTGG 300
QY 1525 ATAAGAAGGGGTGACCAATAGGTACAGATCATTTCTGATGCAAGGGGCTCCAGAGGACC 1584

QY 1424 TTAGCATGGCTTTCAGACCTCAGACATGCTCATCTAATCCTCACAACATGGCTACAGGG 1483
Db 360 TTAGGGATGGCTTTCAGACCTCAGACATGCTCATCTAATCCTCACAACATGGCTACAGGG 419
QY 1484 TGGCACTACTAGCTCCTATTGACAGAGGAAGGACTGTGGATAAAGAGGGGTGACCAA 1543
Db 420 TGGCACTACTAGCTCCTATTGACAGAGGAAGGACTGTGGATAAAGAGGGGTGACCAA 479
QY 1544 TAGTCAGATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1603
Db 480 TAGTCAGATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 539
QY 1604 AGAGAAATTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1663
Db 540 AGAGAAATTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 599
QY 1664 TATCTCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1723
Db 600 TATCTCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 659
QY 1724 ATAATCTCTGCTGCT 1783
Db 660 ATAATCTCTGCTGCT 719
QY 1784 CTCAGCTGGCCAGGTGTAGCCAGTACCTAATCTTTTCAGAGAACTATAAATGTGA 1843
Db 720 CTCAGCTGGCCAGGTGTAGCCAGTACCTAATCTTTTCAGAGAACTATAAATGTGA 779
QY 1844 TCCTACAGGGGAGAAAAAAGAAAGAACTCTGAAAGAGCTGACATTTTACCGACTTGC 1903
Db 780 TCCTACAGGGGAG-AAAAAAGAAAGAACTCTGAAAGAGCTGACATTTTACCGACTTGC 838
QY 1904 ACACATAAGCTAACCTGCCAGTTTGTGCTGGTAGAACTCATGAGACTCCTGGGTGAG 1963
Db 839 ACACATAAGCTAACCTGCCAGTTTGTGCTGGTAGAACTCATGAGACTCCTGGGTGAG 898
QY 1964 GCAAAAGATTTTATACCCAGCTAAGGAGGAGCATGAACTTTGTGTTTCAATTTGTT 2023
Db 899 GCAAAAGATTTTATACCCAGCTAAGGAGGAGCATGAACTTTGTGTTTCAATTTGTT 958
QY 2024 CACTTTGCCCCCAATTCATATGGGATGATCAGAGCAGTTTCAGTGATGACACAGGGG 2083
Db 959 CACTTTGCCCCCAATTCATATGGGATGATCAGAGCAGTTTCAGTGATGACACAGGGG 1018
QY 2084 TTTGTGCAAGGTGAGCAACTAGGCTTGAAGATTCATCTCAATCTTATGAAGAGTACTAG 2143
Db 1019 TTTGTGCAAGGTGAGCAACTAGGCTTGAAGATTCATCTCAATCTTATGAAGAGTACTAG 1078
QY 2144 CAATCTTGTCCAGTCTTGTATCTGCGGAGATATCTTATTAATTTGGTTGAAAGCA 2203
Db 1079 CAATCTTGTCCAGTCTTGTATCTGCGGAGATATCTTATTAATTTGGTTGAAAGCA 1138
QY 2204 GACCTACTCTGGAGGAACATATTTGATTTTATTTGCTGAAAGTAAACAATCTGCTGTA 2263
Db 1139 GACCTACTCTGGAGGAACATATTTGATTTTATTTGCTGAAAGTAAACAATCTGCTGTA 1198
QY 2264 AAATAGAGCTTAATTTATTTATTAAGCAGTAAAGAACTAGATCTGAGGCGATACC 2323
Db 1199 AAATAGAGCTTAATTTATTTATTTATTAAGCAGTAAAGAACTAGATCTGAGGCGATACC 1258
QY 2324 ATCTTGAAGGCTATCTGCTGACAAATATGCTTTGAAAGATGCTCCAGAAAAAGAAACG 2383
Db 1259 ATCTTGAAGGCTATCTGCTGACAAATATGCTTTGAAAGATGCTCCAGAAAAAGAAACG 1318
QY 2384 GTATATTGCTTTGCTCAGAGACACACAGAAACATAGAGAACCATGGAATTTGCT 2443
Db 1319 GTATATTGCTTTGCTCAGAGACACACAGAAACATAGAGAACCATGGAATTTGCT 1378
QY 2444 CCCACACTGTTCCAGGAGCCCTTCCACTCTCTGCTGAGGAGCAGTCTTAAATCCCAT 2503
Db 1379 CCCACACTGTTCCAGGAGCCCTTCCACTCTCTGCTGAGGAGCAGTCTTAAATCCCAT 1438
QY 2504 CATTAGTGTGTCTACCAACATCTGGCTTACCGTCCCTAACCAAGATTTCTAGGTCCAGTT 2563

Db 1439 CATTAGTGTGTCTACCAACATCTGGCTTCCACCGTGCCTAACCAAGATTTCTAGGTCCAGTT 1498
QY 2564 CCCACACTGTTCCAGGAGCCCTTCCACTCTCTGCTGAGGAGCAGTCTTAAATCCCAT 2623
Db 1499 CCCACACTGTTCCAGGAGCCCTTCCACTCTCTGCTGAGGAGCAGTCTTAAATCCCAT 1558
RESULT 13
AXX24774
ID AAX24774 standard; DNA; 1172 BP.
XX
XX AAX24774;
XX AC
XX DT 21-JUN-1999 (first entry)
XX Human glandular kallikrein hKUK2 gene enhancer with mutated ARE.
XX Enhancer; glandular kallikrein-1; hGK-1; hKUK2; human; prostate cancer;
XX therapy; androgen response element; mutant; ss.
XX Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX mutation replace(93.1007, GCAGAAATATCGAAT)
XX /*tag= a
XX /note= "mutated androgen response element"
XX
XX WO9906576-Al.
XX
XX PD 11-FEB-1999.
XX
XX XX 04-AUG-1998; 98WO-US016312.
XX
XX PR 04-AUG-1997; 97US-0054523P.
XX PR 02-MAR-1998; 98US-0076545P.
XX PR 03-AUG-1998; 98US-00127834.
XX
XX (CALY-) CALYDON INC.
XX
XX Yu D, Herdenson DR, Schuur ER;
XX
XX WPI; 1999-153804/13.
XX
XX New nucleic acid containing the human glandular kallikrein enhancer -
XX providing increased expression of heterologous sequences in prostatic
XX cells, and related adenoviral vectors for treating prostatic cancer.
XX
XX Example 7; Page 170; 179pp; English.
XX
XX This polynucleotide is based on nucleotides 7200-8371 of the 5' flanking
XX region of the human glandular kallikrein (hKUK2) gene (see AAX24755), but
XX the putative androgen response element (ARE) of the native sequence (see
XX AAX24772) has been mutated. This mutation was shown to affect the
XX enhancer function of this region of the hKUK2 gene. hKUK2 enhancers of
XX the invention have been shown to increase the transcription of cis-linked
XX coding sequences in prostate cells. Methods of using DNA constructs
XX comprising the enhancers to control transcription of heterologous
XX polynucleotides are provided. Adenoviral vectors in which one or more
XX genes are under transcriptional control of a hKUK2 transcription
XX regulatory element are claimed, and can be used to confer selective
XX cytotoxicity in mammalian cells for use e.g. in the treatment of prostate
XX cancer
XX
XX Sequence 1172 BP; 335 A; 258 C; 268 G; 311 T; 0 U; 0 Other;
XX
XX Query Match 27.2%; Score 993; DB 2; Length 1172;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1225 CAAAGCTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1284

Db	1	CAAAAGCTTAGAGATGACCTCCCAAGGAGCTGAATGCAAAAGACCTGGGCTCTTTGGGCAAG	60
Qy	1285	GAGAACTCTTTACCGCACACTCTCTCTTCACAGGGTTATTGTGAGGATCAAAATGTGGTCAT	1344
Db	61	GAGAACTCTTTACCGCACACTCTCTCTTCACAGGGTTATTGTGAGGATCAAAATGTGGTCAT	120
Qy	1345	GTGTGTGAGACACCAAGACATGTCCTGGCTGTGGAGAGTGACTTCTATGTGTGTAAACATT	1404
Db	121	GTGTGTGAGACACCAAGACATGTCCTGGCTGTGGAGAGTGACTTCTATGTGTGTAAACATT	180
Qy	1405	GCTCAGTGTCTAAGAAAGTTATTAGCATGGCTTTTCAGACACTCACAGATGCTCATCTAATCC	1464
Db	181	GCTCAGTGTCTAAGAAAGTTATTAGCATGGCTTTTCAGACACTCACAGATGCTCATCTAATCC	240
Qy	1465	TCACAAATATGGCTACAGGGTGGGCACACTACTAGCCCTCATTTGACAGAGAAAGGACTGTGG	1524
Db	241	TCACAAATATGGCTACAGGGTGGGCACACTACTAGCCCTCATTTGACAGAGAAAGGACTGTGG	300
Qy	1525	ATAAGAAAGGGGTGACCAATAGGTCAGAGTCATTTCTGGATGCAAGGGGCTCCAGAGACC	1584
Db	301	ATAAGAAAGGGGTGACCAATAGGTCAGAGTCATTTCTGGATGCAAGGGGCTCCAGAGACC	360
Qy	1585	ATGATTAGACATTCCTGTCAGAGAAATATTAGCGTGGATGCTCTGCCCCCGAAAGGGGGA	1644
Db	361	ATGATTAGACATTCCTGTCAGAGAAATATTAGCGTGGATGCTCTGCCCCCGAAAGGGGGA	420
Qy	1645	TGCACCTTTCCCTTGACCCCTATCTCAGATCTTTGAGTTTATCTCAGACTTCCTCT	1704
Db	421	TGCACCTTTCCCTTGACCCCTATCTCAGATCTTTGAGTTTATCTCAGACTTCCTCT	480
Qy	1705	ATGATACAGGAGGCCATCATATCTCTCTGTGTCTCTCTGCCCTTCTCAGTCTTACTGC	1764
Db	481	ATGATACAGGAGGCCATCATATCTCTCTGTGTCTCTCTGCCCTTCTCAGTCTTACTGC	540
Qy	1765	CCACTCTCCAGCTCCATCTCCAGCTGGCCAGGTGTAGCCACAGTACCTTAACTCTTTGC	1824
Db	541	CCACTCTCCAGCTCCATCTCCAGCTGGCCAGGTGTAGCCACAGTACCTTAACTCTTTGC	600
Qy	1825	AGAGAACTATAAATGTGTATCTCTACAGGGGAGAAAAAAGAACTCTGAAAGAGCTG	1884
Db	601	AGAGAACTATAAATGTGTATCTCTACAGGGGAGAAAAAAGAACTCTGAAAGAGCTG	660
Qy	1885	ACATTTTACCGACTTGCAAAACATAGCTTAACTGTCAGTTTGTCTGGTAGAATCA	1944
Db	661	ACATTTTACCGACTTGCAAAACATAGCTTAACTGTCAGTTTGTCTGGTAGAATCA	720
Qy	1945	TGAGACTCTGGGTGACAGGCAAAAGATTTTATTACCCACAGCTTAAGAGGCGACATGAA	2004
Db	721	TGAGACTCTGGGTGACAGGCAAAAGATTTTATTACCCACAGCTTAAGAGGCGACATGAA	780
Qy	2005	CTTTGTGTTTACATTTGTTCACTTTGCCCCCCCAATTCATATGGGATGATCAGAGCAGTTC	2064
Db	781	CTTTGTGTTTACATTTGTTCACTTTGCCCCCCCAATTCATATGGGATGATCAGAGCAGTTC	840
Qy	2065	AGGTGGATGACACAGGGGTTTGTGGCAAGGTGAGCAACTAGGCTTAGAAATCTCTCAA	2124
Db	841	AGGTGGATGACACAGGGGTTTGTGGCAAGGTGAGCAACTAGGCTTAGAAATCTCTCAA	900
Qy	2125	TCTTATAAGAAAGGTACTAGCAAACTGTCAGTCTTTGTATCTGACGAGATATTATCTT	2184
Db	901	TCTTATAAGAAAGGTACTAGCAAACTGTCAGTCTTTGTATCTGACGAGATATTATCTT	960
Qy	2185	TATAATTTGGGTTGAAAGCAGACTTCTCTGGAG	2217
Db	961	TATAATTTGGGTTGAAAGCAGACTTCTCTGGAG	993

DT	21-JUN-1999	(first entry)	
XX	Human glandular kallikrein hKLK2 gene enhancer with mutated ARE.		
XX	Enhancer; glandular kallikrein-1; hGK-1; hKLK2; human; prostate cancer;		
KW	therapy; androgen response element; mutant; ss.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	mutation	replace(993..1007, G T A C T A T A T T A C A G T)	
FT		/*tag= a	
FT		/note= "mutated androgen response element"	
XX			
FN	W09906576-A1.		
PD	11-FEB-1999.		
XX			
PF	04-AUG-1998;	98WO-US016312.	
XX			
FR	04-AUG-1997;	97US-0054523P.	
FR	02-MAR-1998;	98US-0076545P.	
FR	03-AUG-1998;	98US-00127834.	
XX			
PA	(CALY-) CALYDON INC.		
XX			
PI	Yu D, Herdenson DR, Schuur ER;		
XX			
DR	WPI; 1999-153804/13.		
XX			
PT	New nucleic acid containing the human glandular kallikrein enhancer -		
PT	providing increased expression of heterologous sequences in prostatic		
PT	cells, and related adenoviral vectors for treating prostatic cancer.		
XX			
PS	Example 7; page 169; 179pp; English.		
XX			
CC	This polynucleotide is based on nucleotides 7200-8371 of the 5' flanking		
CC	region of the human glandular kallikrein (hKLK2) gene (see AAX24755), but		
CC	the putative androgen response element (ARE) of the native sequence (see		
CC	AAX24772) has been mutated. This mutation was shown to affect the		
CC	enhancer function of this region of the hKLK2 gene. hKLK2 enhancers of		
CC	the invention have been shown to increase the transcription of cis-linked		
CC	coding sequences in prostate cells. Methods of using DNA constructs		
CC	comprising the enhancers to control transcription of heterologous		
CC	polynucleotides are provided. Adenoviral vectors in which one or more		
CC	genes are under transcriptional control of a hKLK2 transcription		
CC	regulatory element are claimed, and can be used to confer selective		
CC	cytotoxicity in mammalian cells for use e.g. in the treatment of prostate		
CC	cancer		
XX			
SQ	Sequence 1172 BP; 334 A; 258 C; 267 G; 313 T; 0 U; 0 Other;		
	Query Match	27.2%; Score 993; DB 2; Length 1172;	
	Best Local Similarity 100.0%; Pred. No. 0;		
	Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1225 CAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCCTCTTTGGGCAAG	1284	
DB	1 CAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCCTCTTTGGGCAAG	60	
QY	1285 GAGAATCCTTTACCGCACATCTCTCCTTTCA CAGGGTTATTGTGAGGATCAAAATGCGTCAT	1344	
DB	61 GAGAATCCTTTACCGCACATCTCTCCTTTCA CAGGGTTATTGTGAGGATCAAAATGCGTCAT	120	
QY	1345 GTGTGTGAGACAC CAGCACATGTCTGCTGTGGAGGTGACTTCTATGTGTGCTTAACATT	1404	
DB	121 GTGTGTGAGACAC CAGCACATGTCTGCTGTGGAGGTGACTTCTATGTGTGCTTAACATT	180	
QY	1405 GCTGAGTGTGAAGAAAGTATTAGCATGTGGCTTTTCAGCACTCA CAGATGCTCATCTAAATCC	1464	
DB	181 GCTGAGTGTGAAGAAAGTATTAGCATGTGGCTTTTCAGCACTCA CAGATGCTCATCTAAATCC	240	

QY 1465 TCACAATGGCTACAGGGGGGCACTAGCTCAATTTGACAGAGGAAGGACTGTGG 1524
PF |||||
XX 241 TCACAACATGGCTACAGGGGGGCACTAGCTCAATTTGACAGAGGAAGGACTGTGG 300
PR |||||
QY 1525 ATAAGAGGGGGTGACCAATAGGTGACAGATCATCTGGATGCAAGGGGCTCCAGAGACC 1584
DB |||||
QY 301 ATAAGAGGGGGTGACCAATAGGTGACAGATCATCTGGATGCAAGGGGCTCCAGAGACC 360
DB |||||
QY 1585 ATGATTAGACATCTCTGACAGAGAAATATGGCTGGATGCTCTGCCCGGAAGGGGA 1644
DB |||||
QY 361 ATGATTAGACATCTCTGACAGAGAAATATGGCTGGATGCTCTGCCCGGAAGGGGA 420
DB |||||
QY 1645 TGCATTTCCCTTGACCCCTATCTCAGATCTTGACATTTGAGGTTATCTCAGACTTCCTCT 1704
DB |||||
QY 421 TGCATTTCCCTTGACCCCTATCTCAGATCTTGACATTTGAGGTTATCTCAGACTTCCTCT 480
DB |||||
QY 1705 ATGATACAGAGCCCATCATATCTCTCTGTCCTCTCCCTTCTCAGTCTTACTGC 1764
DB |||||
QY 481 ATGATACAGAGCCCATCATATCTCTCTGTCCTCTCCCTTCTCAGTCTTACTGC 540
DB |||||
QY 1765 CCACTCTTCCAGCTCCATCTCCAGCTGGCCAGGTGAGCCAGTACCTTAATCTTTTC 1824
DB |||||
QY 541 CCACTCTTCCAGCTCCATCTCCAGCTGGCCAGGTGAGCCAGTACCTTAATCTTTTC 600
DB |||||
QY 1825 AGAAGACTATATGTTGTTATCTTACAGGGGAGAGAAAAAGAACTCTGAAAGAGCTG 1884
DB |||||
QY 601 AGAAGACTATATGTTGTTATCTTACAGGGGAGAGAAAAAGAACTCTGAAAGAGCTG 660
DB |||||
QY 1885 ACATTTTACCGACTTGAACACATAGCTAACTGCTGCTTTGCTGGTAGAACTCA 1944
DB |||||
QY 661 ACATTTTACCGACTTGAACACATAGCTAACTGCTGCTTTGCTGGTAGAACTCA 720
DB |||||
QY 1945 TGAGACTCTTGGGTGAGAGGCAAAAGATTTTATACCCAGCTTAAGGGGCGAGCATGAA 2004
DB |||||
QY 721 TGAGACTCTTGGGTGAGAGGCAAAAGATTTTATACCCAGCTTAAGGGGCGAGCATGAA 780
DB |||||
QY 2005 CTTTGTCTTCACATTTGCTTACCTTGGCCCTCCCAATCATATGAGTATGATGAGTCTC 2064
DB |||||
QY 781 CTTTGTGTTTACATTTGTTTACCTTGGCCCTCCCAATCATATGAGTATGATGAGTCTC 840
DB |||||
QY 2065 AGTGGATGACACAGAGGGGTTTGGCAAGGTTGAGCAACTAGGCTTGAATCTCTCAA 2124
DB |||||
QY 841 AGTGGATGACACAGAGGGGTTTGGCAAGGTTGAGCAACTAGGCTTGAATCTCTCAA 900
DB |||||
QY 2125 TCTTATAGAGGTTACTAGCAACTTGTCCAGTCTTGTATCTGACGGAGATATATCTT 2184
DB |||||
QY 901 TCTTATAGAGGTTACTAGCAACTTGTCCAGTCTTGTATCTGACGGAGATATATCTT 960
DB |||||
QY 2185 TATAATTTGGGTTGAAAGCAGACCTACTCTCTGGAG 2217
DB |||||
QY 961 TATAATTTGGGTTGAAAGCAGACCTACTCTCTGGAG 993
DB |||||

RESULT 15
AAZ06495
ID AAZ06495 standard; DNA; 1172 BP.

XX AC AAZ06495;

XX AC AAZ06495;

XX AC AAZ06495;

XX AC AAZ06495;

XX AC AAZ06495;

XX AC AAZ06495;

XX AC AAZ06495;

XX AC AAZ06495;

XX AC AAZ06495;

XX AC AAZ06495;

XX 11-FEB-1999; 99WO-US003117.
PF |||||
XX 12-FEB-1998; 98US-00022732.
PR |||||
XX (CALY-) CALYDON INC.
PA |||||
XX Henderson DR, Lamparski HG, Schuur ER, Yu DC;
PI WPI; 1999-527378/44.
DB |||||
XX Screening for compounds which inhibit prostate cancer using a cell line
PT containing a marker whose expression is responsive to therapeutically
PF active compounds.
XX Claim 6; Page 50; 50pp; English.
XX This is the nucleotide sequence of the hKLK2 enhancer region contained in
CC construct CN457. hKLK2 is a member of the kallikrein family, as is the
CC prostate specific antigen (PSA), a chymotrypsin like protein that is
CC synthesized exclusively by normal, hyperplastic, and malignant prostatic
CC epithelia. This tissue specific nature of PSA makes it an excellent
CC biomarker for identifying benign prostatic hyperplasia (BPH) and
CC prostatic carcinoma (CaP). Elevated levels of PSA are indicative of BPH
CC or CaP. Like PSA, hKLK2 is expressed exclusively in the prostate and is
CC up regulated by androgens, primarily by transcription activation. The
CC proteins also exhibit a high degree of amino acid sequence identity and
CC contain similar regulatory elements. The characterisation of genes whose
CC expression is limited to the prostate allows the development of screening
CC methods which can identify substances capable of specifically altering
CC the expression of prostate-specific genes
XX SQ Sequence 1172 BP; 334 A; 258 C; 267 G; 313 T; 0 U; 0 Other;

Query Match 27.2%; Score 993; DB 2; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1295 CAAAAGCTTAGAGATGACCTCCAGAGCTGAATGCAAGACCTGTCCTTTGGGCAAG 1284
DB 1 CAAAAGCTTAGAGATGACCTCCAGAGCTGAATGCAAGACCTGTCCTTTGGGCAAG 60
QY 1285 GAGAACTCTTACCCGACACTCTCTCCACAGGGTTATTGTGAGGATCAATGTGGTCAAT 1344
DB 61 GAGAACTCTTACCCGACACTCTCTCCACAGGGTTATTGTGAGGATCAATGTGGTCAAT 120
QY 1345 GTGTGTGAGACACACAGCACATGTCTGGCTGTGGAGAGTACTTCTATGTGCTAAACATT 1404
DB 121 GTGTGTGAGACACACAGCACATGTCTGGCTGTGGAGAGTACTTCTATGTGCTAAACATT 180
QY 1405 GCTGAGTCTGAAGAAAGTATTAGGATGGCTTTCAGCACTCAGAGATGCTCATTAATCC 1464
DB 181 GCTGAGTCTGAAGAAAGTATTAGGATGGCTTTCAGCACTCAGAGATGCTCATTAATCC 240
QY 1465 TCACAACATGGCTACAGGGTGGGCACTACTAGCTCATTTGACAGAGAAAGGACTGTGG 1524
DB 241 TCACAACATGGCTACAGGGTGGGCACTACTAGCTCATTTGACAGAGAAAGGACTGTGG 300
QY 1525 ATAAGAGGGGGTGACCAATAGGTGACAGATCATCTTGGATGCAAGGGGCTCCAGAGACC 1584
DB 301 ATAAGAGGGGGTGACCAATAGGTGACAGATCATCTTGGATGCAAGGGGCTCCAGAGACC 360
QY 1585 ATGATTAGACATTTGCTGACAGAGAAATATGCTGCTGGATGCTCTGCCCGGAAGGGGA 1644
DB 361 ATGATTAGACATTTGCTGACAGAGAAATATGCTGCTGGATGCTCTGCCCGGAAGGGGA 420
QY 1645 TGCATTTCCCTTGACCCCTATCTCAGATCTTGAGGTTATCTCAGACTTCCTCT 1704
DB 421 TGCATTTCCCTTGACCCCTATCTCAGATCTTGAGGTTATCTCAGACTTCCTCT 480
QY 1705 ATGATACAGAGCCCATCATATCTCTCTGTCCTCTCCCTTCTCAGTCTTACTGC 1764
DB 481 ATGATACAGAGCCCATCATATCTCTCTGTCCTCTCCCTTCTCAGTCTTACTGC 540

QY 1765 CCACCTCTCCAGCTCCATCTCCAGCTGGCCAGGTGTAGCCACAGTACCTAACTCTTTGC 1824
DB 541 CCACCTCTCCAGCTCCATCTCCAGCTGGCCAGGTGTAGCCACAGTACCTAACTCTTTGC 600
QY 1825 AGAGAAGCTATATAATGTGTATCTACAGGGGAGAAAAAAGAACTCTGAAGAGCTG 1884
DB 601 AGAGAAGCTATATAATGTGTATCTACAGGGGAGAAAAAAGAACTCTGAAGAGCTG 660
QY 1885 ACATTTACGAGCTGCAACACATAAGCTAACCTGCCAGTTTGTGCTGGTGAAGCTCA 1944
DB 661 ACATTTACGAGCTGCAACACATAAGCTAACCTGCCAGTTTGTGCTGGTGAAGCTCA 720
QY 1945 TGAGACTCTGGGTGACAGGCAAGAAATTTATTTACCCACAGCTAAGGAGGAGCTGAA 2004
DB 721 TGAGACTCTGGGTGACAGGCAAGAAATTTATTTACCCACAGCTAAGGAGGAGCTGAA 780
QY 2005 CTTTGTGTTTACATTTGTTTCACTTTGCCCCCAATTCATATGGATGATCAGAGCAGTTC 2064
DB 781 CTTTGTGTTTACATTTGTTTCACTTTGCCCCCAATTCATATGGATGATCAGAGCAGTTC 840
QY 2065 AGGTGGATGGACACAGGGGTTTGTGGCAAGGTGAGCAACTAGGCTTAGAATCTCTCA 2124
DB 841 AGGTGGATGGACACAGGGGTTTGTGGCAAGGTGAGCAACTAGGCTTAGAATCTCTCA 900
QY 2125 TCTTATAAGAGGTAAGTACTAGCAAACTTGTCCAGTCTTTGTATCTGACGGGAGATATTCTT 2184
DB 901 TCTTATAAGAGGTAAGTACTAGCAAACTTGTCCAGTCTTTGTATCTGACGGGAGATATTCTT 960
QY 2185 TATTAATTTGGGTTGAAAGCAGACCTACTCTGGAG 2217
DB 961 TATTAATTTGGGTTGAAAGCAGACCTACTCTGGAG 993

RESULT 16
AAZ06496
ID AAZ06496 standard; DNA; 1172 BP.
XX AC AAZ06496;
XX DT 23-NOV-1999 (first entry)
XX DE hKlK2 enhancer of construct CN458.
XX KW prostate; cancer; drug assay; drug development; enhancer; promoter;
XX KW tumour; kallikrein; androgen regulation; prostate specific antigen;
XX KW construct; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX FN WO9941413-A2.
XX PD 19-AUG-1999.
XX PF 11-FEB-1999; 99WO-US003117.
XX PR 12-FEB-1998; 98US-00022732.
XX PA (CALY-) CALYDON INC.
XX PI Henderson DR, Lamparski HG, Schuur ER, Yu DC;
XX WPI; 1999-527378/44.
XX PT Screening for compounds which inhibit prostate cancer using a cell line
XX PT containing a marker whose expression is responsive to therapeutically
XX PT active compounds.
XX PS Claim 6; Page 50; 50pp; English.
XX This is the nucleotide sequence of the hKlK2 enhancer region contained in
CC construct CN458. hKlK2 is a member of the kallikrein family, as is the

CC prostate specific antigen (PSA), a chymotrypsin like protein that is
CC synthesized exclusively by normal, hyperplastic, and malignant prostatic
CC epithelia. This tissue specific nature of PSA makes it an excellent
CC biomarker for identifying benign prostatic hyperplasia (BPH) and
CC prostatic carcinoma (Cap). Elevated levels of PSA are indicative of BPH
CC or Cap. Like PSA, hKlK2 is expressed exclusively in the prostate and is
CC up regulated by androgens, primarily by transcription activation. The
CC proteins also exhibit a high degree of amino acid sequence identity and
CC contain similar regulatory elements. The characterisation of genes whose
CC expression is limited to the prostate allows the development of screening
CC methods which can identify substances capable of specifically altering
CC the expression of prostate-specific genes
XX
SQ Sequence 1172 BP; 335 A; 258 C; 268 G; 311 T; 0 U; 0 Other;
Query Match 27.2%; Score 993; DB 2; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1225 CAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCTCTTTGGGCAAG 1284
DB 1 CAAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCTCTTTGGGCAAG 60
QY 1285 GAGAACTCTTTACCGACACTCTCTTACAGAGTTATTTGTAGGATCAAAATGTGTCAT 1344
DB 61 GAGAACTCTTTACCGACACTCTCTTACAGAGTTATTTGTAGGATCAAAATGTGTCAT 120
QY 1345 GTGTGTGAGACACAGACATGCTGGCTGTGGAGAGTGACTTCTATGTGTCTAATTC 1404
DB 121 GTGTGTGAGACACAGACATGCTGGCTGTGGAGAGTGACTTCTATGTGTCTAATTC 180
QY 1405 GCTGAGTCTTAAGAAAGTATTAGGCATGGCTTTACAGCACTCACAGATGCTCTAATTC 1464
DB 181 GCTGAGTCTTAAGAAAGTATTAGGCATGGCTTTACAGCACTCACAGATGCTCTAATTC 240
QY 1465 TCACAGATGCTACAGGTGGGCACTACTAGCTCTATTTACAGAGGAAGGACTCTGG 1524
DB 241 TCACAGATGCTACAGGTGGGCACTACTAGCTCTATTTACAGAGGAAGGACTCTGG 300
QY 1525 ATAAGAGGGGTGACCAATAGGTGAGATGATCTCTGGATGCAAGGGGCTCCAGAGGACC 1584
DB 301 ATAAGAGGGGTGACCAATAGGTGAGATGATCTCTGGATGCAAGGGGCTCCAGAGGACC 360
QY 1585 ATGATTAGACATTTGTGTCAGAGAAATTTAGGCTGGATGCTCTGCCCCGGAAGGGGGA 1644
DB 361 ATGATTAGACATTTGTGTCAGAGAAATTTAGGCTGGATGCTCTGCCCCGGAAGGGGGA 420
QY 1645 TGCATTTCTTGTACCCCTATCTCAGATCTTGACTTTGAGGTTATCTCAGACTTCTCTCT 1704
DB 421 TGCATTTCTTGTACCCCTATCTCAGATCTTGACTTTGAGGTTATCTCAGACTTCTCTCT 480
QY 1705 ATGATACAGAGGCCCATCATATCTCTGTGTCTCTCCCTTCTCAGTCTTACTGC 1764
DB 481 ATGATACAGAGGCCCATCATATCTCTGTGTCTCTCCCTTCTCAGTCTTACTGC 540
QY 1765 CCACCTCTCCAGCTCCATCTCCAGCTGGCCAGGTGTAGCCACAGTACCTAACTCTTTGC 1824
DB 541 CCACCTCTCCAGCTCCATCTCCAGCTGGCCAGGTGTAGCCACAGTACCTAACTCTTTGC 600
QY 1825 AGAGAAGCTATATAATGTGTATCTCTACAGGGGAGAAAAAAGAACTCTGAAGAGCTG 1884
DB 601 AGAGAAGCTATATAATGTGTATCTCTACAGGGGAGAAAAAAGAACTCTGAAGAGCTG 660
QY 1885 ACATTTACGAGCTGCAACACATAAGCTAACCTGCCAGTTTGTGCTGGTGAAGCTCA 1944
DB 661 ACATTTACGAGCTGCAACACATAAGCTAACCTGCCAGTTTGTGCTGGTGAAGCTCA 720
QY 1945 TCAGACTCTGGGTGACAGGCAAGAAATTTATTTACCCACAGCTAAGGAGGAGCAGCTGAA 2004
DB 721 TGAGACTCTGGGTGACAGGCAAGAAATTTATTTACCCACAGCTAAGGAGGAGCAGCTGAA 780
QY 2005 CTTTGTGTTTACATTTGTTTCACTTTGCCCCCAATTCATATGGATGATCAGAGCAGTTC 2064

Db 781 CTTTGGTTTTCACATTTGTTTCACTTTCCTCCCTCCCAATTCATATGGAATGATCAGAGCAGTTC 840
QY 2065 AGGTGGATGACACACGGGTTTGTGCAAAAGGTGAGCAACCTAGGCTTAGAAATCCTCAA 2124
Db 841 AGGTGGATGACACACGGGTTTGTGCAAAAGGTGAGCAACCTAGGCTTAGAAATCCTCAA 900
QY 2125 TCTTATAAGAAGTACTAGCAACTTGTCCAGTCTTGTATCTGACGGAGATATTATCTT 2184
Db 901 TCTTATAAGAAGTACTAGCAACTTGTCCAGTCTTGTATCTGACGGAGATATTATCTT 960
QY 2185 TATAATTGGGTTGAAAGCAGACCTACTCTGGAG 2217
Db 961 TATAATTGGGTTGAAAGCAGACCTACTCTGGAG 993

RESULT 17

AAF82694
ID AAF82694 standard; DNA; 204 BP.

XX AAF82694;

XX 18-JUN-2001 (first entry)

XX Glandular HK2 enhancer core sequence.

XX Androgen response element; ARE; cytostatic; gene therapy;
XX prostate-specific chimeric enhancer; transcriptional regulation;
XX targeted gene expression; prostate cancer; prostate disorder;
XX prostate-specific antigen; PSA; glandular HK2; ds.

XX Unidentified.

XX WO200127256-A2.

XX 19-APR-2001.

XX 13-OCT-2000; 2000WO-US028444.

XX 14-OCT-1999; 99US-0159691P.

XX 15-OCT-1999; 99US-0159730P.

XX (REGC) UNIV CALIFORNIA SYSTEM.

XX Wu L, Carey MF, Belidegrun AS;

XX WPI; 2001-273768/28.

XX New polynucleotide, useful for treating prostatic cancer, comprises
XX prostate specific chimeric enhancer and proximal promoter sequence.
XX operably linked to nucleic acid encoding heterologous polypeptide.

XX Claim 17; Page 80; 13pp; English.

XX The present sequence may be used in an invention relating to an isolated
XX polynucleotide comprising a prostate-specific chimeric enhancer (PSE)
XX sequence and a proximal promoter sequence operably linked to a nucleic
XX acid segment that encodes a heterologous polypeptide. The PSE contains an
XX ARE and specifically activates transcription of the nucleic acid segment
XX in a mammalian prostate cell. The construct is useful for the treatment
XX of a prostate disorder or a metastasised prostate cancer, such as
XX hyperplasia or hyperproliferation of prostate cells. It is also useful
XX for directing the tissue-specific expression of a heterologous
XX polypeptide in a human prostate cell. The construct may be administered
XX by injection, infection, transformation, liposome-mediated transfection,
XX polybrene-mediated transfection, receptor-mediated uptake or Ca-P04-
XX mediated transformation

XX Sequence 204 BP; 67 A; 34 C; 39 G; 64 T; 0 U; 0 Other;

XX Query Match 5.6%; Score 204; DB 5; Length 204;

XX Best Local Similarity 100.0%; Pred. NO. 7.9e-88;

XX Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2158 CTTTGTATCTGACGGATATTATCTTTATAATTGGCTTGAAGCAGACCTACTCTGGAG 2217
Db 1 CTTTGTATCTGACGGATATTATCTTTATAATTGGCTTGAAGCAGACCTACTCTGGAG 60
QY 2218 GAACATATTCTATTATTGTCCTGACAGTAACAAATCTGCTGTAAAAATAGACGTTTAAAC 2277
Db 61 GAACATATTGTTATTATTGTCCTGACAGTAACAAATCTGCTGTAAAAATAGACGTTTAAAC 120
QY 2278 TTTTATTATCTAAGCAGTAAGCAACCTAGATCTGAAGGCGATACCATCTTGCAAGGCTA 2337
Db 121 TTTTATTATCTAAGCAGTAAGCAACCTAGATCTGAAGGCGATACCATCTTGCAAGGCTA 180
QY 2338 TCTGCTGTACAAATATGCTTGAAA 2361
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Job time : 1303 secs

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Job time : 8672 secs

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OM nucleic - nucleic search, using sw model
Run on: August 10, 2004, 13:51:43 ; Search time 8672 Seconds
(without alignments)
12551.620 Million cell updates/sec

Title: US-09-875-228-1_COPY_5976_9620
Perfect score: 3645
Sequence: 1 GGccctcaataattgttaag.....ggaggaggctgtggactggc 3645

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 150

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 250 summaries

- Database : EST.*
- 1: em_estba.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estmu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_htc.*
 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_htc.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: em_gss_hum.*
 - 18: em_gss_inv.*
 - 19: em_gss_pin.*
 - 20: em_gss_vrt.*
 - 21: em_gss_fun.*
 - 22: em_gss_mam.*
 - 23: em_gss_mus.*
 - 24: em_gss_pro.*
 - 25: em_gss_rpd.*
 - 26: em_gss_phg.*
 - 27: em_gss_vri.*
 - 28: gb_gss1.*
 - 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result	Query		
No.	Score	Match Length DB ID	Description

No matches found			

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2004, 13:51:43 ; Search time 13686 Seconds
(without alignments)
11543.574 Million cell updates/sec

Title: US-09-875-228-1_COPY_5976_9620

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 150

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 250 summaries

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3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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21: em_or:*
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23: em_pat:*
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26: em_ro:*
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28: em_un:*
29: em_vi:*
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31: em_htg_inv:*
32: em_htg_other:*
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35: em_htg_rod:*
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37: em_htg_vrt:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3645	100.0	12047	6	AR266428	AR266428 Sequence
3	3645	100.0	12047	6	AX259951	AX259951 Sequence
4	3645	100.0	12047	6	AX262356	AX262356 Sequence
5	3645	100.0	12047	6	BD195482	BD195482 Adenoviru
6	3645	100.0	12047	6	BD224259	BD224259 Adenoviru
7	3645	100.0	12282	9	AF113169	AF113169 Homo sapi
8	2750	75.4	40458	9	AC011523	AC011523 Homo sapi
9	2750	75.4	217346	2	AC027602	AC027602 Homo sapi
10	2750	75.4	230000	9	AF243527	AF243527 Homo sapi
11	1626	44.6	34560	9	AC037199	AC037199 Homo sapi
12	1369	37.6	5002	9	AF174646	AF174646 Homo sapi
13	1172	32.2	1172	6	AR078696	AR078696 Sequence
14	993	27.2	1172	6	AR078697	AR078697 Sequence
15	993	27.2	1172	6	AR078698	AR078698 Sequence
16	171	4.7	203	6	AX113818	AX113818 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AR078691 12047 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5964371.
ACCESSION AR078691
VERSION AR078691.1 GI:10005437
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12047)
AUTHORS McCabe,R.Paul.
TITLE Disposable reservoir for evaporative coolers
JOURNAL Patent: US 5964371-A 1 12-OCT-1999;
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 3645; DB 6; Length 12047;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5976 GGCCTCAATTAATGTTAAGAGTGTAAATGTTCCAGAGATGGAATAATGTTTGAGAACTA 6035
QY 61 CTGTCCAGAGATTTCTGTAGTTCTAGAGTGTGGGAATATAGAACCTGGAGCTTGGCTT 120
Db 6036 CTGTCCAGAGATTTCTGTAGTTCTAGAGTGTGGGAATATAGAACCTGGAGCTTGGCTT 6095
QY 121 CTTGAGCCTAGAAATCAGGAGTATGGGCTGAGTCTGAGCTTGGCTTTCACAGCTTGGG 180
Db 6096 CTTGAGCCTAGAAATCAGGAGTATGGGCTGAGTCTGAGCTTGGCTTTCACAGCTTGGG 6155
QY 181 GTTGGCTTCCGAGCACAATATTGACATGTTGCGACTGTGTATTTGGGTTTGGTATTTC 240
Db 6156 GTTGGCTTCCGAGCACAATATTGACATGTTGCGACTGTGTATTTGGGTTTGGTATTTC 6215
QY 241 TCTGAATCCTAATGTCCTCTTGGGCAATCTAGAAATCTGAAATCTGTGGTCAAGATTCT 300
Db 6216 TCTGAATCCTAATGTCCTCTTGGGCAATCTAGAAATCTGAAATCTGTGGTCAAGATTCT 6275

Pred. No. is the number of results predicted by chance to have a

301 ATTATCTTGAGTAGGACATCTCCAGTCTCTGGTTCTGCTTCTAGGCGTGGAGTCTGTAGT 360
6276 ATATCTTGAGTAGGACATCTCCAGTCTCTGGTTCTGCTTCTAGGCGTGGAGTCTGTAGT 6335
361 CAGTGACCCCGGTCTGGCAATTTCAACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 420
6336 CAGTGACCCCGGTCTGGCAATTTCAACTTCATATACAGTGGGCTATCTTTTGGTCCATGTTT 6395
421 CAACCAACACCGAAATTAACCACTTAGAACCTTTCCCACTTCCCTAGCTGCAATGTTAA 480
6396 CAACCAACACCGAAATTAACCACTTAGAACCTTTCCCACTTCCCTAGCTGCAATGTTAA 6455
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6456 ACCTAGGATTTCTGTTTAAATAGGTTTCATATGAATTAATTTTCCAGCTGATCCAACTTTACAT 5515
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6516 TCCTTCTACCGTTATTTCTACACCCACCTTAAATGCAATTTCCCAATATATTTCCCTGGATT 6575
601 CTACCTATATAGTAAATCTGGCTTTGCCAGTTTCTAGTGCATTAACATACCTGATTTA 660
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6636 CATTCCTTTTACTTTAAAGTGGAAATAGAGTCCCTCTGCAGAGTTTCCAGAGTTTCTCAAGA 6695
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7296 ATTGTGAGGATCAAAATGTGTCATGTGTGTGAGACACAGCATGTCTGGCTGTGGAGA 7355
1381 GTGACTTCTATGTGTCTAAACATTTGCTGAGTGTCTAAGAAAGTATTAGGCATGGCTTTTCAG 1440

7356 GTGACTTCTATGTGTCTAAACATTTGCTGAGTCTAAGAAAGTATTAGGCATGGCTTTTCAG 7415
1441 CACTCACAGATGCTCATCTAATCTCACAACATGGCTACAGGTGGGCACTACTAGCCTC 1500
7416 CACTCACAGATGCTCATCTAATCTCACAACATGGCTACAGGTGGGCACTACTAGCCTC 7475
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RESULT 2
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LOCUS AR266428 12047 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 11 from patent US 6495130.
ACCESSION AR266428
VERSION AR266428.1 GI:29695384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 12047)
AUTHORS Henderson,D.R. and Yu,D.C.
TITLE Target cell-specific adenoviral vectors containing E3 and methods
of use thereof
JOURNAL Patent: US 6495130-A 11 17-DEC-2002;
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Db 6036 CTGTCCCAAGATTTCTCTGAGTTCTAGAGTGTGGGATATAGAACCTGGAGCTTGGCTT 6095
Qy 121 CTTAGCCCTAGAAATCAGGAGTATGGGCTGAAGCTCTGAAGCTTGGCTTCAGCAGTTTGGG 180
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Qy	1981	CCAGCTTAAGGAGCGACATGAACTTTGTGTTACATTTGTTACATTTGCCGCCCAATT	2040
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AX259951
LOCUS 12047 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 36 from Patent WO0172341.
ACCESSION AX259951
VERSION AX259951.1 GI:16509011
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
Yt, D.C., Chen, Y., and Henderson, D.R.
AUTHORS Methods of treating neoplasia with combinations of target
TITLE cell-specific adenovirus, chemotherapy and radiation
JOURNAL Patent: WO 0172341-A 36 04-OCT-2001;
Calydon, Inc. (US)

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Db	6456	ACCTAGGATTTCTGTTTAATAGGTTTCAATGAATAATTTGAGCTGTATCCCACTTTACAT	6515
QY	541	TCCTTCTACCGTTTATTTTACACCACTTAAATAATGCAATCCCAATATATTTCCCTGGATT	600
Db	6516	TCCTTCTACCGTTTATTTTACACCACTTAAATAATGCAATCCCAATATATTTCCCTGGATT	6575
QY	601	CTACCTATATATGTTAATTCCTGGCTTTGCCAGTTTCTAGTGCATTAACATACCTGATTTA	660
Db	6576	CTACCTATATATGTTAATTCCTGGCTTTGCCAGTTTCTAGTGCATTAACATACCTGATTTA	6635
QY	661	CATTCTTTTACTTTAAGTGAATAAGAGTCCCTCTGCAGAGTTCAGAGTCTCTCAAGA	720
Db	6636	CATTCTTTTACTTTAAGTGAATAAGAGTCCCTCTGCAGAGTTCAGAGTCTCTCAAGA	6695
QY	721	TGGCCCTTACTTCTGACATCAATTCAGATTTTCAAGGAGTGCCTCAAGATCATCTCAGGT	780
Db	6696	TGGCCCTTACTTCTGACATCAATTCAGATTTTCAAGGAGTGCCTCAAGATCATCTCAGGT	6755
QY	781	TCAGTGATGCTGGTAGCCCTCATATACCTCAATGAAGCTGTTATGCTCATGGCTATGG	840
Db	6756	TCAGTGATGCTGGTAGCCCTCATATACCTCAATGAAGCTGTTATGCTCATGGCTATGG	6815
QY	841	TTTATTACAGCAAAAGATAGAGATGAAATCTAGCAAGGAGAGAGTTCATGGGGGCAAA	900
Db	6816	TTTATTACAGCAAAAGATAGAGATGAAATCTAGCAAGGAGAGAGTTCATGGGGGCAAA	6875
QY	901	GACAAGGAGAGCTCCAGAGTGCAGAGATTCCTGTTGTTTCTCCAGTGGTGTCTATGGAAA	960

Db 6876 GACAAAGAGAGCTCCAAAGTGACAGAGATCTCTGTGTGTTTCTCCAGTGGTGTATGAA 6935
Qy 961 GCAGTATCTTCTCCATACAAATGATGTGTGATAATATTAGTGTATTTGCCAATCAGGGAAC 1020
Db 6936 GCAGTATCTTCTCCATACAAATGATGTGTGATAATATTAGTGTATTTGCCAATCAGGGAAC 6995
Qy 1021 TCAACTGAGCTTGAATATATTGGAGCTTGGTTGCACAGACATGTGCACACCTTCATGG 1080
Db 6996 TCAACTGAGCTTGAATATATTGGAGCTTGGTTGCACAGACATGTGCACACCTTCATGG 7055
Qy 1081 CTGAACCTTTAGTACTAGCCCTCCAGACGCTCTACAGCTGATAGGCTGTAAACCAACATT 1140
Db 7056 CTGAACCTTTAGTACTAGCCCTCCAGACGCTCTACAGCTGATAGGCTGTAAACCAACATT 7115
Qy 1141 GTCAACATAATACATTTGTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 1200
Db 7116 GTCAACATAATACATTTGTAGACTATCCAGTGTGGCCCAAGCTCCCGTGTAAACACAG 7175
Qy 1201 GCACCTTAAACAGCAGCATATTTCAAAGCTTAGAGATGACCTCCAGAGCTGAATGC 1260
Db 7176 GCACCTTAAACAGCAGCATATTTCAAAGCTTAGAGATGACCTCCAGAGCTGAATGC 7235
Qy 1261 AAAGACCTGGCTCTTTGGGCAAGGAAATCTTTACCGCACACTCTCCCTTCAACAGGTT 1320
Db 7236 AAAGACCTGGCTCTTTGGGCAAGGAAATCTTTACCGCACACTCTCCCTTCAACAGGTT 7295
Qy 1321 ATTGTGAGGATCAAACTGTGTGATGTGTGAGACACACGACATCTCTGGCTGTGGAG 1380
Db 7296 ATTGTGAGGATCAAACTGTGTGATGTGTGAGACACACGACATCTCTGGCTGTGGAG 7355
Qy 1381 GTGACTTCTATGTGTGATTAACATTTGCTGAGTGTGTAAAGAGTATTAGGATGGCTTTTCAG 1440
Db 7356 GTGACTTCTATGTGTGATTAACATTTGCTGAGTGTGTAAAGAGTATTAGGATGGCTTTTCAG 7415
Qy 1441 CACTACAGATGCTCATCTAATCTCTCAACATGGCTACAGGTTGGGCTACTAGCCTC 1500
Db 7416 CACTACAGATGCTCATCTAATCTCTCAACATGGCTACAGGTTGGGCTACTAGCCTC 7475
Qy 1501 ATTTGACAGAGGAAGGACTGTGGATAAGAAAGGGGTGACCAATAGGTGACAGTCAATCT 1560
Db 7476 ATTTGACAGAGGAAGGACTGTGGATAAGAAAGGGGTGACCAATAGGTGACAGTCAATCT 7535
Qy 1561 GGATGCAAGGGCTCCAGAGGACCATGATTAGACATTTGCTGACAGAGAAATTATGGCTGG 1620
Db 7536 GGATGCAAGGGCTCCAGAGGACCATGATTAGACATTTGCTGACAGAGAAATTATGGCTGG 7595
Qy 1621 ATGTCTCTGCCCGAAAGGGGATGCATTTCTTGACCCCTATCTCAGATCTTTGACT 1680
Db 7596 ATGTCTCTGCCCGAAAGGGGATGCATTTCTTGACCCCTATCTCAGATCTTTGACT 7655
Qy 1681 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGACCATATTAATCTCTGTGTGC 1740
Db 7656 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGACCATATTAATCTCTGTGTGC 7715
Qy 1741 TCTCCCTCTCTCAGTCTTACTGCCACTCTCCAGCTCCATCTCCAGCTGGCCAGGTTG 1800
Db 7716 TCTCCCTCTCTCAGTCTTACTGCCACTCTCCAGCTCCATCTCCAGCTGGCCAGGTTG 7775
Qy 1801 TAGCCACAGTACCTTAATCTTTGACAGAACTATAATGTATCTCAGAGGAGAGAAA 1860
Db 7776 TAGCCACAGTACCTTAATCTTTGACAGAACTATAATGTATCTCAGAGGAGAGAAA 7835
Qy 1861 AAAAAAGAACTGGAAGAGCTGACATTTTACCGACTTGCACACATAGCTAACCTG 1920
Db 7836 AAAAAAGAACTGGAAGAGCTGACATTTTACCGACTTGCACACATAGCTAACCTG 7895
Qy 1921 CCAGTTTGTGCTGGTAGAACTCATGAGACTCTCTGGGTGAGAGGCAAAAGATTTATTAC 1980
Db 7896 CCAGTTTGTGCTGGTAGAACTCATGAGACTCTCTGGGTGAGAGGCAAAAGATTTATTAC 7955
Qy 1981 CCAGCTTAAGGAGGACGATGAATTTGTGTTTCAATTTGCTTTCATTTGCCCCCAATT 2040

Db 7956 CCACAGCTAAGAGGACGATGAATTTGTGTTTCAATTTGTTTCACTTTGCCCCCAATT 8015
Qy 2041 CATATGGGATGATCAGAGCAGTTTCAAGTGTGATGACACAGGGTTTGTGCAAGGTGAG 2100
Db 8016 CATATGGGATGATCAGAGCAGTTTCAAGTGTGATGACACAGGGTTTGTGCAAGGTGAG 8075
Qy 2101 CAACCTAGGCTTAGAAATCTCATCTTATAAGAGGCTACTAGCAACTTTGTCAGTCTT 2160
Db 8076 CAACCTAGGCTTAGAAATCTCATCTTATAAGAGGCTACTAGCAACTTTGTCAGTCTT 8135
Qy 2161 TGTATCTGACGAGATATTATCTTTATAATTGGGTTGAAAGCAGACCTACTCTGGAGAA 2220
Db 8136 TGTATCTGACGAGATATTATCTTTATAATTGGGTTGAAAGCAGACCTACTCTGGAGAA 8195
Qy 2221 CATATTTGATTTATTTGCTGACAGTAACAAATCTGCTGTAAATAGACGTTAACTTT 2280
Db 8196 CATATTTGATTTATTTGCTGACAGTAACAAATCTGCTGTAAATAGACGTTAACTTT 8255
Qy 2281 ATTATCTAAGGACGTAAGCAAACTAGATCTGAAGGCGATACCATCTTTGCAAGGCTATCT 2340
Db 8256 ATTATCTAAGGACGTAAGCAAACTAGATCTGAAGGCGATACCATCTTTGCAAGGCTATCT 8315
Qy 2341 GCTGTACAAATATGCTTTGAAAGATGCTCCAGAAAGAAACCGTATTTATTTGCTTTGCT 2400
Db 8316 GCTGTACAAATATGCTTTGAAAGATGCTCCAGAAAGAAACCGTATTTATTTGCTTTGCT 8375
Qy 2401 CAGAAGACACACAGAAACATAGAGAACCATGGAATTTGCTCCCAAACTGTTCAACC 2460
Db 8376 CAGAAGACACACAGAAACATAGAGAACCATGGAATTTGCTCCCAAACTGTTCAACC 8435
Qy 2461 AGAGCTTTCCACTCTTTGTCAGGACAGTCTTAAACATCCCATATTTAGTGTGTACCA 2520
Db 8436 AGAGCTTTCCACTCTTTGTCAGGACAGTCTTAAACATCCCATATTTAGTGTGTACCA 8495
Qy 2521 CATCTGGCTTCACTGCTTAAACCAAGATTTCTAGGTCAGTTCCCAACCATGTTGGCA 2580
Db 8496 CATCTGGCTTCACTGCTTAAACCAAGATTTCTAGGTCAGTTCCCAACCATGTTGGCA 8555
Qy 2581 GTGCCCCCCTGCCAACCCAGAAATAGGGAGTGTCTAGAAATTCGAGGGGACATGGTGG 2640
Db 8556 GTGCCCCCCTGCCAACCCAGAAATAGGGAGTGTCTAGAAATTCGAGGGGACATGGTGG 8615
Qy 2641 GGATCAGAACTTCTGGGCTTGAAGTGCAGAGGGGCGCATCTCTCTGTTCCGAAGGAG 2700
Db 8616 GGATCAGAACTTCTGGGCTTGAAGTGCAGAGGGGCGCATCTCTCTGTTCCGAAGGAG 8675
Qy 2701 AAGAGGCTGAGGTTGAATGTCTTTGGAGGGAGAAATGTGGGTTCTGAACTCTTAATCC 2760
Db 8676 AAGAGGCTGAGGTTGAATGTCTTTGGAGGGAGAAATGTGGGTTCTGAACTCTTAATCC 8735
Qy 2761 CCAAGGGAGGAGACTGGTAAAGTCCAGCTTCCAGGTTCTGAGTGTGGAAATGGCTGAG 2820
Db 8736 CCAAGGGAGGAGACTGGTAAAGTCCAGCTTCCAGGTTCTGAGTGTGGAAATGGCTGAG 8795
Qy 2821 AGGCTTAAGAAATCCGTTATCTCGGGAAGCAGGGGCTGAAATGTGAGGGGTTGAGTTC 2880
Db 8796 AGGCTTAAGAAATCCGTTATCTCGGGAAGCAGGGGCTGAAATGTGAGGGGTTGAGTTC 8855
Qy 2881 AGGGTTTGTGAGCTTGTGAGACTCTCTGGTGGTCTCGGGGAAGCAAGGACTGGAACCAT 2940
Db 8856 AGGGTTTGTGAGCTTGTGAGACTCTCTGGTGGTCTCGGGGAAGCAAGGACTGGAACCAT 8915
Qy 2941 GGCTCCAGGGTTTGGTGTGAAGTAAATGGGATCTCTGATTTCTCAAGGGTCAAGGACT 3000
Db 8916 GGCTCCAGGGTTTGGTGTGAAGTAAATGGGATCTCTGATTTCTCAAGGGTCAAGGACT 8975
Qy 3001 GAGAGTTTCCCATCTTTGATCTTTCCATCTACTCTTCTTCTTCTTCTTCTTCTTCTTCT 3060
Db 8976 GAGAGTTTCCCATCTTTGATCTTTCCATCTACTCTTCTTCTTCTTCTTCTTCTTCTTCT 9035
Qy 3061 TACTCTTCTAGTTCCACAGAGTCCGCTCGGAGTGAATTAATCTGACATGTCCTCATGTC 3120
Db 9036 TACTCTTCTAGTTCCACAGAGTCCGCTCGGAGTGAATTAATCTGACATGTCCTCATGTC 9095

QY	1201	GCACCTCTAAACAGGACGATATTTCAAAAGCTTAGAGATGACCTCCACGAGCTGAATGC	1260
Db	7176	GCACCTCTAAACAGGACGATATTTCAAAAGCTTAGAGATGACCTCCACGAGCTGAATGC	7235
QY	1261	AAAGACCTGGGCTCTTTGGGCAAGGAGAAATCCCTTTACCGCACACTCTCTTCAAGGGTT	1320
Db	7236	AAAGACCTGGGCTCTTTGGGCAAGGAGAAATCCCTTTACCGCACACTCTCTTCAAGGGTT	7295
QY	1321	ATTGTGAGGATCAAAATGTGTGATGTGTGAGACACACACATGTCGGCTGTGAGAA	1380
Db	7296	ATTGTGAGGATCAAAATGTGTGATGTGTGAGACACACACATGTCGGCTGTGAGAA	7355
QY	1381	GTGACTTCTATGTGTGCTAACATTTGCTGAGTGTCTAAGAAAGTATTAGGCATGGCTTTTCAG	1440
Db	7356	GTGACTTCTATGTGTGCTAACATTTGCTGAGTGTCTAAGAAAGTATTAGGCATGGCTTTTCAG	7415
QY	1441	CACCTACAGATGCTCATCTAATCTCTCAACATGGCTACAGGGTGGGCACTACTAGCCCTC	1500
Db	7416	CACCTACAGATGCTCATCTAATCTCTCAACATGGCTACAGGGTGGGCACTACTAGCCCTC	7475
QY	1501	ATTTGACAGAGAAAGGACTGTGATAGAGGGGGTGACCAATAGGTACAGATCTATTCT	1560
Db	7476	ATTTGACAGAGAAAGGACTGTGATAGAGGGGGTGACCAATAGGTACAGATCTATTCT	7535
QY	1561	GGATGCAAGGGCTCCAGAGGACCATGATTAGACATTTGCTGAGAGAAATTAGGCTGG	1620
Db	7536	GGATGCAAGGGCTCCAGAGGACCATGATTAGACATTTGCTGAGAGAAATTAGGCTGG	7595
QY	1621	ATGTCTCTGCCCCGGAAAGGGGATGACATTTCTTGAACCCCTATCTCAGATCTTTGACT	1680
Db	7596	ATGTCTCTGCCCCGGAAAGGGGATGACATTTCTTGAACCCCTATCTCAGATCTTTGACT	7655
QY	1681	TTGAGGTTAICTCAGACTTCTCTATGATACAGAGGACCATCATATCTCTCTGTGTC	1740
Db	7656	TTGAGGTTAICTCAGACTTCTCTATGATACAGAGGACCATCATATCTCTCTGTGTC	7715
QY	1741	TCTCCCTCTCTCAGTCTTACTGCCACTCTTCCAGCTCCATCTCCAGCTGCCAGGTC	1800
Db	7716	TCTCCCTCTCTCAGTCTTACTGCCACTCTTCCAGCTCCATCTCCAGCTGCCAGGTC	7775
QY	1801	TAGCCACAGTACCTTAATCTTTGACAGAACTATAATGTGTATCTCAGGGGAGAAAA	1860
Db	7776	TAGCCACAGTACCTTAATCTTTGACAGAACTATAATGTGTATCTCAGGGGAGAAAA	7835
QY	1861	AAAAAAGAACTCTGAAGAGCTGACATTTTACGGACTTGCACACATAGCTAACCTG	1920
Db	7836	AAAAAAGAACTCTGAAGAGCTGACATTTTACGGACTTGCACACATAGCTAACCTG	7895
QY	1921	CCAGTTTGTGCTGGTAGAACTCATGAGACTCTCGGGTCAGAGGCAAAAGATTTATTAC	1980
Db	7896	CCAGTTTGTGCTGGTAGAACTCATGAGACTCTCGGGTCAGAGGCAAAAGATTTATTAC	7955
QY	1981	CCAGCTTAGGCTAGAGGACGATGAACTTTGTGTTTCACTTTGCTCCCTCCCTCCCT	2040
Db	7956	CCAGCTTAGGCTAGAGGACGATGAACTTTGTGTTTCACTTTGCTCCCTCCCTCCCT	8015
QY	2041	CATATGGGATGATCAGAGCACTTTCAGTGTGATGGACACACAGGGGTTTGTGGCAAGGTGAG	2100
Db	8016	CATATGGGATGATCAGAGCACTTTCAGTGTGATGGACACACAGGGGTTTGTGGCAAGGTGAG	8075
QY	2101	CAACCTAGGCTTAGAATCTCAATCTTATAGAGGATCTAGCAACCTTGTCTCAGTCTT	2160
Db	8076	CAACCTAGGCTTAGAATCTCAATCTTATAGAGGATCTAGCAACCTTGTCTCAGTCTT	8135
QY	2161	TGTATCTGACCGAGATATTTATCTTTTATATTTGGGTTGAAAGCAGACCTACTCTGAGGAA	2220
Db	8136	TGTATCTGACCGAGATATTTATCTTTTATATTTGGGTTGAAAGCAGACCTACTCTGAGGAA	8195
QY	2221	CATATTTGATTTATGCTGAAACAGTAAACAAATCTGCTGTAAATAGACGTTAACTTT	2280
Db	8196	CATATTTGATTTATGCTGAAACAGTAAACAAATCTGCTGTAAATAGACGTTAACTTT	8255
QY	2281	ATTATCTAAGGACGTAAAGCAACCTTAGATCTGAGGCGATACCATCTTCCAGGCTATCT	2340

Db	8256	ATTATCTAAGGACGTAAAGCAACCTTAGATCTGAGGCGATACCATCTTTCAGAGGCTATCT	8315
QY	2341	GCTGTACAAATATGCTTCAAAAGATGCTCCAGAAAGAAAAACGATATTTATTTGCCTTTGCT	2400
Db	8316	GCTGTACAAATATGCTTCAAAAGATGCTCCAGAAAGAAAAACGATATTTATTTGCCTTTGCT	8375
QY	2401	CAGAGACACACAGAAACATTAAGAGAACCATGGAAATTTGCTCCCAACATGTTCCACC	2460
Db	8376	CAGAGACACACAGAAACATTAAGAGAACCATGGAAATTTGCTCCCAACATGTTCCACC	8435
QY	2461	AGAGCCTTCCACTCTTGTCTCAGGACAGTCTTAACATCCCATCATTTAGTGTGTCTACCA	2520
Db	8436	AGAGCCTTCCACTCTTGTCTCAGGACAGTCTTAACATCCCATCATTTAGTGTGTCTACCA	8495
QY	2521	CATCTGGCTTCAACGCTGCTTAACCAAGATTTCTAGTCCAGTTCCCAACCATGTTTGCCA	2580
Db	8496	CATCTGGCTTCAACGCTGCTTAACCAAGATTTCTAGTCCAGTTCCCAACCATGTTTGCCA	8555
QY	2581	GTGCCCTCACTGCCAACCCACAGATAAAGGAGTGTCTCAGAAATTCGAGGGGACATGGGTGG	2640
Db	8556	GTGCCCTCACTGCCAACCCACAGATAAAGGAGTGTCTCAGAAATTCGAGGGGACATGGGTGG	8615
QY	2641	GGATCAGAACTTCTGGGCTTGAGTGCAGAGGGGGCCCATACTCTCTGGTCCGAGAGAGG	2700
Db	8616	GGATCAGAACTTCTGGGCTTGAGTGCAGAGGGGGCCCATACTCTCTGGTCCGAGAGAGG	8675
QY	2701	AAGAGGCTGGAGGTGAATGTCTTTGGAGGGGAGGAAATGTGGGTTCTCAACTCTTAAATCC	2760
Db	8676	AAGAGGCTGGAGGTGAATGTCTTTGGAGGGGAGGAAATGTGGGTTCTCAACTCTTAAATCC	8735
QY	2761	CCAGGGAGGAGACGTGTAGTCCAGCTTCCAGGTCTCCAGGTACTGAGCTGGGAAATGGCTTCG	2820
Db	8736	CCAGGGAGGAGACGTGTAGTCCAGCTTCCAGGTCTCCAGGTACTGAGCTGGGAAATGGCTTCG	8795
QY	2821	AGGTCTTAGAATCCCGTATCTCCGGAGGAGGGGCTGAAATTTGAGAGGGTTGAGTTGC	2880
Db	8796	AGGTCTTAGAATCCCGTATCTCCGGAGGAGGGGCTGAAATTTGAGAGGGTTGAGTTGC	8855
QY	2881	AGGGTTTGTGTAGCTTGAGACTCTCTGGTGGGTCCTCGGAAAGCAAGGACTGGAACCAT	2940
Db	8856	AGGGTTTGTGTAGCTTGAGACTCTCTGGTGGGTCCTCGGAAAGCAAGGACTGGAACCAT	8915
QY	2941	GGCTCCAGGGTTGGTGTGAAGTAAATGGGATCTCTGATTTCTCAAGGGTCTAGAGGACT	3000
Db	8916	GGCTCCAGGGTTGGTGTGAAGTAAATGGGATCTCTGATTTCTCAAGGGTCTAGAGGACT	8975
QY	3001	GAGAGTTGCCCATCTTTTGATCTTTCCATCTTACTCTTACTTCCACTTTGAGGGTAAATCACC	3060
Db	8976	GAGAGTTGCCCATCTTTTGATCTTTCCATCTTACTCTTACTTCCACTTTGAGGGTAAATCACC	9035
QY	3061	TACTCTTCTAGTTCCACAGAGTGGCTTCGGGAGTAAATCTGACATGTGCCATGTC	3120
Db	9036	TACTCTTCTAGTTCCACAGAGTGGCTTCGGGAGTAAATCTGACATGTGCCATGTC	9095
QY	3121	CCGAGGCTTGGGATCATCATCTCATCTTCCATCTGCGTATGCGGGGCGAGGCGGG	3180
Db	9096	CCGAGGCTTGGGATCATCATCTCATCTTCCATCTGCGTATGCGGGGCGAGGCGGG	9155
QY	3181	CGCCATGAGCTCATGTAGTGGCATATCTCTGAGGCGGCTCTCCCTGTCAGCTGCCCAA	3240
Db	9156	CGCCATGAGCTCATGTAGTGGCATATCTCTGAGGCGGCTCTCCCTGTCAGCTGCCCAA	9215
QY	3241	CCATGGAGCTTGGACGCTGGCTCCCTGGTGGATGTGGCTGCGTGGTCCAGCGCGGG	3300
Db	9216	CCATGGAGCTTGGACGCTGGCTCCCTGGTGGATGTGGCTGCGTGGTCCAGCGCGGG	9275
QY	3301	CCTGGTCTCGATTAAGATCTTAGAACCCAGAGAAACAGGACTGAAAGTGTCTAGAGAA	3360
Db	9276	CCTGGTCTCGATTAAGATCTTAGAACCCAGAGAAACAGGACTGAAAGTGTCTAGAGAA	9335
QY	3361	TGGCCATATCTGCTGCTCCATGAATCTCAAGACTTCTGGGTGGAGGCGCACAGGAGCT	3420

QY 1261 AAGACCTGGCTCTTTGGCAAGAGAAATCCTTTACCGCACACTCTCTCTTCACAGGCTT 1320
Db 7236 AAGACCTGGCTCTTTGGCAAGAGAAATCCTTTACCGCACACTCTCTCTTCACAGGCTT 7295
QY 1321 ATTGTGAGATCAAAATGCTGTCATGCTGTGTGAGACACACACATGCTGTGGCTGTGAGA 1380
Db 7236 ATTGTGAGATCAAAATGCTGTCATGCTGTGTGAGACACACACATGCTGTGGCTGTGAGA 7355
QY 1381 GTGACTTCTATGTGTGCTAAACATGCTGAGTGTCTAAGAAAGTATTAGGCATGGCTTTCAG 1440
Db 7356 GTGACTTCTATGTGTGCTAAACATGCTGAGTGTCTAAGAAAGTATTAGGCATGGCTTTCAG 7415
QY 1441 CACTCAGAGATGCTCATCTATCTCTCAACATGGCTACAGGGTGGGACACTACTAGGCTC 1500
Db 7416 CACTCAGAGATGCTCATCTATCTCTCAACATGGCTACAGGGTGGGACACTACTAGGCTC 7475
QY 1501 ATTTGACAGAGAAAGGACTGTGGATAAGAAAGGGGTGACCAATAGGTTCAGAGTCATTCT 1560
Db 7476 ATTTGACAGAGAAAGGACTGTGGATAAGAAAGGGGTGACCAATAGGTTCAGAGTCATTCT 7535
QY 1561 GGATCGAAGGGCTCCAGAGAGACCATGATTTAGACATTTGCTGACAGAAATATGCTGG 1620
Db 7536 GGATCGAAGGGCTCCAGAGAGACCATGATTTAGACATTTGCTGACAGAAATATGCTGG 7595
QY 1621 ATGTCTCTGCCCCGGAAGGGGGATGCACTTTTCCTTGACCCCTATCTCAGATCTTGACT 1680
Db 7596 ATGTCTCTGCCCCGGAAGGGGGATGCACTTTTCCTTGACCCCTATCTCAGATCTTGACT 7655
QY 1681 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCCCATATATCTCTCTGTGTC 1740
Db 7656 TTGAGGTTATCTCAGACTTCTCTATGATACAGAGGCCCATATATCTCTCTGTGTC 7715
QY 1741 TCTCCCTTCTCAGTCTTACTGCCCCACTCTCCAGCTCCATCTCCAGTGGCCAGGTG 1800
Db 7716 TCTCCCTTCTCAGTCTTACTGCCCCACTCTCCAGCTCCATCTCCAGTGGCCAGGTG 7775
QY 1801 TAGCCACAGTAACTCTTTTGACAGAACTATAAATGTGTATCCTACAGGGGAGAAA 1860
Db 7776 TAGCCACAGTAACTCTTTTGACAGAACTATAAATGTGTATCCTACAGGGGAGAAA 7835
QY 1861 AAAAAAGAACTGAAAGAGCTGACATTTTACCGACTTGCRAACACATAGCTTAACCTG 1920
Db 7836 AAAAAAGAACTGAAAGAGCTGACATTTTACCGACTTGCRAACACATAGCTTAACCTG 7895
QY 1921 CCAGTTTGTGCTGGTAGAACTCATGAGCTCTCTGGGTGAGGCAAAAGATTTTATTAC 1980
Db 7896 CCAGTTTGTGCTGGTAGAACTCATGAGCTCTCTGGGTGAGGCAAAAGATTTTATTAC 7955
QY 1981 CCACAGTAAAGGGCAGCATGAATTTGTGTTTCAATTTGTTTCACTTTGCCCCCAAT 2040
Db 7956 CCACAGTAAAGGGCAGCATGAATTTGTGTTTCAATTTGTTTCACTTTGCCCCCAAT 8015
QY 2041 CATATGGATGATCAGAGCAGTTTCAAGTGGATGACACAGGGGTTTGTGCAAGGTGAG 2100
Db 8016 CATATGGATGATCAGAGCAGTTTCAAGTGGATGACACAGGGGTTTGTGCAAGGTGAG 8075
QY 2101 CAACCTAGGCTTAAATCTCTAATCTTATAGAAGGTACTAGCAAACTTGTCCAGTCTT 2160
Db 8076 CAACCTAGGCTTAAATCTCTAATCTTATAGAAGGTACTAGCAAACTTGTCCAGTCTT 8135
QY 2161 TGTATCTGACGGAGATTTATCTTTATTTGTTTGAAGCAGACTACTCTGAGGAA 2220
Db 8136 TGTATCTGACGGAGATTTATCTTTATTTGTTTGAAGCAGACTACTCTGAGGAA 8195
QY 2221 CATATGTTATTTATGCTGAACAGTAAACAAATCTGCTGTAATAATAGACGTTTAACTTT 2280
Db 8196 CATATGTTATTTATGCTGAACAGTAAACAAATCTGCTGTAATAATAGACGTTTAACTTT 8255
QY 2281 ATTATCTAGGCAAGTAAACCTAGATCTGAGGCGATACCACTTTGCAAGGCTATCT 2340
Db 8256 ATTATCTAGGCAAGTAAACCTAGATCTGAGGCGATACCACTTTGCAAGGCTATCT 8315

QY 2341 GCTGTACAAATATGCTTGAAGAGATGCTCCAGAAAGAAACGGTATTATTGCTCTTGTCT 2400
Db 8316 GCTGTACAAATATGCTTGAAGAGATGCTCCAGAAAGAAACGGTATTATTGCTCTTGTCT 8375
QY 2401 CAGAGACACACAGAAACATATAGAGAACCATGGAATAATGCTCTCCAAACATGTTTCAACC 2460
Db 8376 CAGAGACACACAGAAACATATAGAGAACCATGGAATAATGCTCTCCAAACATGTTTCAACC 8435
QY 2461 AGAGCCTTCCACTCTGCTGTCAGACAGTCTTAAACATCCCATCATTTAGTGTGTACCA 2520
Db 8436 AGAGCCTTCCACTCTGCTGTCAGACAGTCTTAAACATCCCATCATTTAGTGTGTACCA 8495
QY 2521 CATCTGGCTTCACTGCTTAAACAGATTTCTAGTCCAGTTCCTCCACCATGTTTGCA 2580
Db 8496 CATCTGGCTTCACTGCTTAAACAGATTTCTAGTCCAGTTCCTCCACCATGTTTGCA 8555
QY 2581 GTGCCCACTGCCAACCCAGAAATAGGAGTGTCTCAGAAATCCAGAGGGACATGGGTGG 2640
Db 8556 GTGCCCACTGCCAACCCAGAAATAGGAGTGTCTCAGAAATCCAGAGGGACATGGGTGG 8615
QY 2641 GGATCAGAACTTCTGGGCTTGTGTCAGAGGGGCCCATACTCTCTTGGTCCGAAGGAGG 2700
Db 8616 GGATCAGAACTTCTGGGCTTGTGTCAGAGGGGCCCATACTCTCTTGGTCCGAAGGAGG 8675
QY 2701 AAGAGCTGGAGGTAATGCTCTTGGAGGGAGGAATGCTGGTCTGAACCTTTAAATCC 2760
Db 8676 AAGAGCTGGAGGTAATGCTCTTGGAGGGAGGAATGCTGGTCTGAACCTTTAAATCC 8735
QY 2761 CCAAGGGAGGAGACTGTGTAAGTCTCCAGCTTCCAGGTACTGAGTGGGAATGSCCTGAG 2820
Db 8736 CCAAGGGAGGAGACTGTGTAAGTCTCCAGCTTCCAGGTACTGAGTGGGAATGSCCTGAG 8795
QY 2821 AGGTCTAAGAACTCCGTAATCTCTCGGAAGGAGGGGCTGAAATTTGTAGGGGTGAGTTC 2880
Db 8796 AGGTCTAAGAACTCCGTAATCTCTCGGAAGGAGGGGCTGAAATTTGTAGGGGTGAGTTC 8855
QY 2881 AGGGTTTGTGTAGCTTGTAGACTCTCTGGTGGGTCCCTGGGAAGCAAGACTTGAACCAT 2940
Db 8856 AGGGTTTGTGTAGCTTGTAGACTCTCTGGTGGGTCCCTGGGAAGCAAGACTTGAACCAT 8915
QY 2941 GGCTCAGGGTTTGGTGTGAAGGTAAATGGGATCTCTGATTTCTCAAGGGTCAAGGACT 3000
Db 8916 GGCTCAGGGTTTGGTGTGAAGGTAAATGGGATCTCTGATTTCTCAAGGGTCAAGGACT 8975
QY 3001 GAGAGTCCCATGCTTTGATCTTTCCATCTTACCTTCTTCTTCTTCAAGGGTCAAGGACT 3060
Db 8976 GAGAGTCCCATGCTTTGATCTTTCCATCTTACCTTCTTCTTCTTCAAGGGTCAAGGACT 9035
QY 3061 TACTCTTCTAGTTCCAAAGAGTGCCTCTGGGAGTATAATCTGCAATGTGCAATGTG 3120
Db 9036 TACTCTTCTAGTTCCAAAGAGTGCCTCTGGGAGTATAATCTGCAATGTGCAATGTG 9095
QY 3121 CCGAGGCTGGGACATCATCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3180
Db 9096 CCGAGGCTGGGACATCATCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 9155
QY 3181 CGCCATGAGCTCATGTAGCTGCGACTATCCCTGAGCGCCCTCTCCCTGCAAGTCCCAA 3240
Db 9156 CGCCATGAGCTCATGTAGCTGCGACTATCCCTGAGCGCCCTCTCCCTGCAAGTCCCAA 9215
QY 3241 CCATGGAGCTGTGGAGCTGGTCCCTGCTGGATGTGGCTGGTGGTGGTGGTGGTGGTGGTGG 3300
Db 9216 CCATGGAGCTGTGGAGCTGGTCCCTGCTGGATGTGGCTGGTGGTGGTGGTGGTGGTGG 9275
QY 3301 CCTGGTGTCCGATAAAGATCCTAGAACACAGGAAACACAGGACTGAAAGGTGTAGAGAA 3360
Db 9276 CCTGGTGTCCGATAAAGATCCTAGAACACACAGGAAACACAGGACTGAAAGGTGTAGAGAA 9335
QY 3361 TGGCCATATGTCCGTGTCCATGAATCTCAAGGACTTCTGGGTGGAGGGACAGGAGCCT 3420
Db 9336 TGGCCATATGTCCGTGTCCATGAATCTCAAGGACTTCTGGGTGGAGGGACAGGAGCCT 9395
QY 3421 GAACTTACGGGTTTGGCCCCAGTCCACTGTCTCTCCCAAGTGTCTCCAGATACGAGGCA 3480

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LOCUS BD224259 12047 bp DNA linear PAT 17-JUL-2003
DEFINITION Adenovirus vectors containing cell status-specific response
elements and methods of use thereof.
ACCESSION BD224259
VERSION BD224259.1 GI:33034029
KEYWORDS JP 2002525063-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 12047)
AUTHORS Yu, D.C. and Henderson, D.R.
TITLE Adenovirus vectors containing cell status-specific response
elements and methods of use thereof
JOURNAL Patent: JP 2002525063-A 5 13-AUG-2002;
CALYDON INC
COMMENT OS Homo sapiens (human)
PN JP 2002525063-A/5
PD 13-AUG-2002
PF 10-SEP-1999 JP 2000570347
PR 10-SEP-1998 US 60/097991, 09-SEP-1999 US 09/392822 P1
DE CHAO YU, DANIEL R HENDERSON
PC C12N15/09, A61K48/00, A61P35/00, C12N1/15, C12N1/19, C12N1/21, C12N5/PC
10, C12N7/02//A61K35/76, C12N15/00, C12N5/00
CC Adenovirus vectors containing cell status-specific response
elements and
CC methods of use thereof
FH Key Location/Qualifiers
FT source 1..12047
FT /organism='Homo sapiens (human)'.
FEATURES
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Query Match 100.0%; Score 3645; DB 6; Length 12047;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
AF113169
LOCUS AF113169 12282 bp DNA linear PRI 05-MAY-1999
DEFINITION Homo sapiens glandular kallikrein enhancer region, complete
SEQUENCE.
ACCESSION AF113169
VERSION AF113169.1 GI:4164598
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 12282)
YU, D.C., Sakamoto, G.T. and Henderson, D.R.
Identification of the transcriptional regulatory sequences of human
kallikrein 2 and their use in the construction of calydon virus
764, an attenuated replication competent adenovirus for prostate
cancer therapy
Cancer Res. 59 (7), 1498-1504 (1999)
JOURNAL
MEDLINE 99211477
PUBMED 10197620
REFERENCE 2 (bases 1 to 12282)
YU, D.C., Sakamoto, G.T. and Henderson, D.R.
Direct Submission
TITLE Submitted (14-DEC-1998) Research, Calydon Inc., 1324 Chesapeake
Terrace, Sunnyvale, CA 94089, USA
JOURNAL
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LOCUS Homo sapiens chromosome 19 clone LLNLF-214C7, complete sequence.

AC011523

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HTG.

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 40458)

TITLE Direct Submission

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 40458)

TITLE Direct Submission

AUTHORS DOE Joint Genome Institute.

JOURNAL Direct Submission

REFERENCE 3 (bases 1 to 40458)

TITLE Direct Submission

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

JOURNAL Direct Submission

COMMENT Submitted (07-OCT-1999): Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Submitted (28-JUN-2000): DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jun 28, 2000 this sequence version replaced gi:7690159.

Draft Sequence produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.sggc.stanford.edu

Quality: Phrap Quality >=40 100% of Sequence;

Estimated Total Number of Errors is 0.

SFS Content:

WT-9055 G07097.

FEATURES

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VERSION
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 217346)
Biren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhvalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
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Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lanazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
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Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,K., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 217346)
Biren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavskiy,L.,
Boukhvalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collimore,A., Cooke,P.,
DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G.,
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Morrow,J., Murphy,T., Naylor,K., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riback,M., Riley,R.,
Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 15, 2000 this sequence version replaced gi:11136831.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center

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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIER
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L9166
Center clone name: 795_B_6
----- Summary Statistics
Sequencing vector: M13; M7815; 31% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 210748 bases at least Q40
Consensus quality: 213655 bases at least Q30
Consensus quality: 215058 bases at least Q20
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Insert size: 216246; sum-of-contigs
Quality coverage: 11.9 in Q20 bases; agarose-fp
Quality coverage: 10.7 in Q20.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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DEFINITION AF243527
ACCESSION AF243527.1 GI:11244757
VERSION AF243527.1
KEYWORDS
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 230000)
AUTHORS Gan, L., Lee, I., Smith, R., Argonza-Barrett, R., Lei, H., McCuaig, J.,
Moss, P., Paepker, B. and Wang, K.
TITLE Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region
JOURNAL Gene 257 (1), 119-130 (2000)
MEDLINE 20510030
PUBMED 11054574
REFERENCE 2 (bases 1 to 230000)
AUTHORS Moss, P., Paepker, B. and Wang, K.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) Chiroscience R & D Inc., 1631 220th St. SE,
Bothell, WA 98021, USA
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Qy      1741  TCTCCCTTCTCAGTCTTATCTGCCACTCTTCCAGCTCCATCTCCAGCTGGCCAGGTG 1800
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number of bases overlapped is 8570.

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Db	2040	TGTCGCTGTCATCAATCTCAAGGACTTCTGGGTGAGGGCCACAGAGCTGAACCTTAC	2099
QY	3429	GGGTTTGCCCGAGTCCACTGTCTCCCAAGTGAAGTCTCCAGATACAGGCACTGTGCCA	3488
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ACCESSION	AF174646		
VERSION	AF174646.1	GI:9957030	
KEYWORDS			
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 5002)		
TITLE	Mitchell, S.H., Murcha, P.E., Zhang, S., Zhu, W. and Young, C.Y.		
JOURNAL	An androgen-response element mediates LNCaP cell dependent androgen induction of the hK2 gene		
MEDLINE	Mol. Cell. Endocrinol. 168 (1-2), 89-99 (2000)		
PUBMED	20519385		
REFERENCE	2 (bases 1 to 5002)		
AUTHORS	Young, C.Y.F., Murtha, P.E. and Mitchell, S.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-AUG-1999) Urology, Mayo Clinic/Foundation, 200 1st St. SW, Rochester, MN 55905, USA		
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QY	1250	GAGCTGAATCAAAGACCTGGCCTCTTTGGCAAGGAGAACTCTTTACCGCACACTCTCC	1309

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AUTHORS			
McCabe, R. Paul.			
TITLE			
Disposable reservoir for evaporative coolers			
JOURNAL			
Patent: US 5964371-A 6 12-OCT-1999;			
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RESULT 14
AR078697

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Qy	1705	ATGATACAGGAGCCCATCAATCTCTCTGTGCTCTCTCCCTTCTCTCAGTCTTACTGC	1764
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Qy	1765	CCACTCTTCCAGCTCCCATCTCCAGCTGGCAGGTGTAGCCACAGTACTTAACTCTTTC	1824
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Qy	1825	AGAGAACTATAAATGTGTATCTCAGGGGAGAAAAAAGAACTCTTGAAGAGCTG	1884
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Db	661	ACATTTTACCGACTTGCACACATAGCTACCTGCCAGTTTCTGTGGTGTAGAACTCA	720
Qy	1945	TGAGACTCTGTGGTGTGAGGCAAAAGATTTTATTAACCAAGCTAAGAGGAGCATGAA	2004
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Qy	2065	AGGTGATGTGACACAGGGGTTTGTGGCAAGGTGAGCAACCTTAGGCTTTAGAAATCCTCAA	2124
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Qy	2185	TATAATTGGGTTGAAAGCAGACCTACTCTGGAGGAAATATTTGTATTTATTTCTCTGAAC	2244
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Qy	2245	AGTAAACAAATCTGTGTAAATAGACGTTTAACTTTATTTATCTAAGGAGGTAAAGCAACC	2304
Db	1021	AGTAAACAAATCTGTGTAAATAGACGTTTAACTTTATTTATCTAAGGAGGTAAAGCAACC	1080
Qy	2305	TAGTCTGAGGCGATACCATCTTGCAGGCTATCTGCTGTACAATATGCTTTGAAAGA	2364
Db	1081	TAGTCTGAGGCGATACCATCTTGCAGGCTATCTGCTGTACAATATGCTTTGAAAGA	1140
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Db	1141	TGGTCCAGAAAAAAGGATTTATTTGCTT	1172

LOCUS AR078697 1172 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 7 from patent US 5964371.
ACCESSION AR078697
VERSION AR078697.1 GI:10005443
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1172)
Mc Cabe, R. Paul.
TITLE Disposable reservoir for evaporative coolers
JOURNAL Patent: US 5964371-A 7 12-OCT-1999;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1285 GAGATCCTTTACCGCACACTCTCTTACAGGGTTATTGTGAGGATCAAAATGTGGTCAT 1344
Db 61 GAGATCCTTTACCGCACACTCTCTTACAGGGTTATTGTGAGGATCAAAATGTGGTCAT 120
QY 1345 GTGTGTGAGACACAGACATGCTGTGCTGTGGAGAGTACTTCTATGTGCTAACTT 1404
Db 121 GTGTGTGAGACACAGACATGCTGTGCTGTGGAGAGTACTTCTATGTGCTAACTT 180
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RESULT 15

AR078698
LOCUS AR078698 1172 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 8 from patent US 5964371.
ACCESSION AR078698
VERSION AR078698.1 GI:10005444
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1172)
AUTHORS McCabe, R. Paul.
TITLE Disposable reservoir for evaporative coolers
JOURNAL Patent: US 5964371-A 8 12-OCT-1999;
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 27.2%; Score 993; DB 6; Length 1172;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 993; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1225 CAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCTCTTTGGGCAAG 1284
Db 1 CAAAGCTTAGAGATGACCTCCAGGAGCTGAATGCAAGACCTGGCTCTTTGGGCAAG 60
QY 1285 GAGATCCTTTACCGCACACTCTCTTACAGGGTTATTGTGAGGATCAAAATGTGGTCAT 1344
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Db 241 TCACAACATGGCTACAGGTTGGGCACTACTAGCTCTATTTGACAGAGAAAGGACTGTGG 300
QY 1525 ATAGAGAGGGGTGACCAATAGGTCAGAGTCTTGGATGCAAGGGCTCCAGAGACC 1584
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QY 1585 ATGATTAGACATTTCTGCGAGAGAAATATGGTGTGATGCTCTGCCCGGAAAGGGGGA 1644
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Search completed: August 11, 2004, 01:15:47
Job time : 13695 secs

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DB 961 TATAATGGGTTGAAAGCAGACCTACTCTGGAG 993

RESULT 16
AX113818
LOCUS AX113818 203 bp DNA linear PAT 01-MAY-2001
DEFINITION Sequence 64 from Patent WO0127256.
ACCESSION AX113818
VERSION AX113818.1 GI:13939984
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Wu, L., Carey, M. F. and Beldegrun, A. S.
TITLE ChimERIC transcriptional regulatory element and methods for
prostate-targeted gene expression
JOURNAL Patent: WO 0127256-A 64 19-APR-2001;
The Regents of the University of California System (US)
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